



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 168510

TO: Bennett Celsa
Location: REM-2A252C18
Art Unit: 1639
Monday, July 11, 2005
Case Serial Number: 09/748739

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Celsa,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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FMS 8

1/8 02p
158510
Access DB#

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: BENNETT CELSA Examiner #: 73815 Date: 7/9/05
Art Unit: 1139 Phone Number 305-7556 Serial Number: 09/748,739
Mail Box and Bldg/Room Location: REMSEN Results Format Preferred (circle): PAPER DISK E-MAIL
2018

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched, include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Butyryl choline esterase Inhibitor

Inventors (please provide full names):

Earliest Priority Filing Date:

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

PERFORM SEQ SEARCH

1. 29-602 SEQ ID #2

wherein position 356 = Tryptophan (w)

Please note: Seq ID 2 already has tryptophan at 356. No editing

2. INTERf SEARCH was required.

29-602 SEQ ID #2

356 → TRYPTOPHAN

see ATTACHED claim 1

Please Rush

I approve

Mr
JEFFREY FREDMAN
PRIMARY EXAMINER

Thanks

Ex CELSR

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 11:11:07 ; Search time 77 Seconds
(without alignments)
2883.123 Million cell updates/sec

Title: US-09-748-739a-2_COPY_29_602

Perfect score: 3110

Sequence: 1 EDDIIATKNGKVRGNLTV.....MDWKQNFNDYTSKESCVGL 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A: Genesep 16Dec04:*

1: Genesep1980s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3110	100.0	574	7	ABW00722 Human but
2	3110	100.0	602	5	AAO18977 Human but
3	3107	99.9	574	8	ADRO1039 Human but
4	3103	99.8	574	8	ADRO1047 Human but
5	3102	99.7	574	8	ADRO1051 Human but
6	3102	99.7	574	8	ADRO1035 Human but
7	3101	99.7	574	8	ADRO1041 Human but
8	3100	99.7	574	8	ADRO1037 Human but
9	3099	99.6	574	5	AAO18944 Human but
10	3098	99.6	574	8	ADRO1049 Human but
11	3096	99.5	574	5	AAE25235 Human but
12	3096	99.5	574	5	AAO18982 Human but
13	3096	99.5	574	5	AAO18988 Human but
14	3096	99.5	574	6	ABR62391 Human but
15	3096	99.5	574	7	ABW00695 Human but
16	3096	99.5	574	8	ADP44639 Human but
17	3096	99.5	574	8	ADRO1077 Human but
18	3096	99.5	602	3	AAV59235 Human but
19	3096	99.5	602	3	AAV49471 Human but
20	3096	99.5	602	3	AAV4573 Human but
21	3096	99.5	602	6	ABR62392 Human but
22	3096	99.5	602	7	ADP90308 Human but
23	3095	99.5	574	8	ADRO1045 Human but
24	3093	99.5	574	8	ADRO1059 Human but
25	3093	99.5	574	8	ADRO1075 Human but

26	3092	99.4	574	5	AAO18977 Human but
27	3092	99.4	574	7	ABW00722 Human but
28	3092	99.4	574	8	ADRO1080 Human but
29	3092	99.4	602	3	AAV44574 Human but
30	3091	99.4	574	5	AAO18979 Human but
31	3091	99.4	574	5	AAO18980 Human but
32	3091	99.4	602	3	AAV49483 Human but
33	3090	99.4	574	5	AAO18983 Human but
34	3090	99.4	574	5	AAO18945 Human but
35	3090	99.4	574	8	ADP44833 Human but
36	3090	99.4	574	8	ADRO1073 Human but
37	3090	99.4	602	2	AAE37442 Full-length
38	3089	99.3	574	5	AAO18981 Human but
39	3089	99.3	574	5	AAO18940 Human but
40	3089	99.3	574	8	ADRO1079 Human but
41	3089	99.3	574	8	ADRO1078 Human but
42	3089	99.3	602	3	AAV49474 Human but
43	3089	99.3	602	3	AAV49473 Human but
44	3089	99.3	602	3	AAV49475 Human but
45	3088	99.3	574	7	ABW00724 Human but

ALIGNMENTS

RESULT 1

ABW00722

ID ABW00722 standard; protein; 574 AA.

XX AC ABW00722;

XX DT 15-JAN-2004 (first entry)

XX DE Human butyrylcholinesterase variant protein (A328W).

XX KW Human; butyrylcholinesterase; enzyme; mutant; mutein; variant.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 328

XX FT /note= "Wild-type Ala substituted with Trp"

XX PN US2003096401-A1.

XX PD 22-MAY-2003.

XX PF 28-NOV-2001; 2001US-00997209.

XX PR 28-NOV-2000; 2000US-0367370P.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX DR WPI; 2003-786991/74.

Cell composition comprises non-yeast eukaryotic cells having diverse population of variant nucleic acids or heterologous nucleic acid fragments, useful for identifying polypeptide with optimized activity.

Example 11; Page; Opp; English.

The invention relates to a cell composition comprising a population of non-yeast eukaryotic cells containing diverse population of variant nucleic acids, or heterologous nucleic acid fragments with distinct species of nucleic acid fragments, where each of the variant nucleic acids or heterologous nucleic acid fragments are expressed in different cell and located within each cell at an identical site in the genome. The invention is useful for identifying polypeptide with optimised activity and for identifying a polypeptide receptor for a ligand. The present sequence is human butyrylcholinesterase variant protein. This sequence is

CC used in the exemplification of the invention. Note: This sequence is not
CC shown in the specification but is derived from the human
CC butyrylcholinesterase wild-type protein (ABW00695) shown in figure 8 of
CC the specification
XX
SQ Sequence 574 AA;

```
Query Match      100.0%; Score 3110; DB 7; Length 574;
Best Local Similarity 100.0%; Pred. No. 2.3e-278;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDDIIITKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRRLRFKKPQSLTKWSDIMNATK 60
Db 1 EDDIIITKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRRLRFKKPQSLTKWSDIMNATK 60

Qy 61 YANSCCNIDQSPFGHSEMNNTDLSDCILYNWIPAPKPNATVLIWYGGGFQT 120
Db 61 YANSCCNIDQSPFGHSEMNNTDLSDCILYNWIPAPKPNATVLIWYGGGFQT 120

Qy 121 GTSSLHVYDGFKLARVERVIVSMNRYRGALGFALPGNPEAPGNMGLFDQQLALQWVQK 180
Db 121 GTSSLHVYDGFKLARVERVIVSMNRYRGALGFALPGNPEAPGNMGLFDQQLALQWVQK 180

Qy 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy 241 NRTLNKLATGCSRENETEIIKCLRNDKDPQOILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Db 241 NRTLNKLATGCSRENETEIIKCLRNDKDPQOILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

Qy 301 DMPDILLELQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Db 301 DMPDILLELQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360

Qy 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYFNFCPALFETTKFSEWGNNAFFYY 420
Db 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYFNFCPALFETTKFSEWGNNAFFYY 420

Qy 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISVKRWANFAKYNP 480
Db 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISVKRWANFAKYNP 480

Qy 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDEAE 540

Qy 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574
```

RESULT 2
AAO18897
ID AAO18897 standard; protein; 602 AA.
XX
AC AAO18897;
XX
DT 02-DEC-2002 (first entry)
XX
XX Human butyrylcholinesterase variant #1.
DE
KW Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
KW cocaine addiction; antiaddictive; antidote.
XX
OS Homo sapiens.
XX
FN WO200264796-A2.
XX
PD 22-AUG-2002.
XX
PF 21-DEC-2001; 2001WO-US050450.
XX

```
PR 26-DEC-2000; 2000US-00748739.  
PR 20-DEC-2001; 2001US-00032233.  
XX  
PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.  
PA (UYNE-) UNIV NEBRASKA MEDICAL CENT.  
XX  
PI Lockridge O, Watkins JD, Pancook JD;  
XX  
DR MPI; 2002-636633/68.  
DR N-PSDB; AAL49276.  
XX  
XX New human butyrylcholinesterase variant polypeptides, useful for treating  
PT cocaine-induced conditions.  
XX  
PS Claim 1; Fig 1; 150pp; English.  
XX  
CC The present invention relates to mutants of human butyrylcholinesterase.  
CC The enzymes have an increased cocaine hydrolysis activity and can be used  
CC for treating a cocaine-induced condition. The present sequence is a  
CC protein shown in the exemplification of the invention  
XX  
SQ Sequence 602 AA;
```

```
Query Match      100.0%; Score 3110; DB 5; Length 602;
Best Local Similarity 100.0%; Pred. No. 2.5e-278;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDDIIITKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRRLRFKKPQSLTKWSDIMNATK 60
Db 29 EDDIIITKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRRLRFKKPQSLTKWSDIMNATK 88

Qy 61 YANSCCNIDQSPFGHSEMNNTDLSDCILYNWIPAPKPNATVLIWYGGGFQT 120
Db 89 YANSCCNIDQSPFGHSEMNNTDLSDCILYNWIPAPKPNATVLIWYGGGFQT 148

Qy 121 GTSSLHVYDGFKLARVERVIVSMNRYRGALGFALPGNPEAPGNMGLFDQQLALQWVQK 180
Db 149 GTSSLHVYDGFKLARVERVIVSMNRYRGALGFALPGNPEAPGNMGLFDQQLALQWVQK 208

Qy 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268

Qy 241 NRTLNKLATGCSRENETEIIKCLRNDKDPQOILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Db 269 NRTLNKLATGCSRENETEIIKCLRNDKDPQOILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328

Qy 301 DMPDILLELQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Db 329 DMPDILLELQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 388

Qy 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYFNFCPALFETTKFSEWGNNAFFYY 420
Db 389 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYFNFCPALFETTKFSEWGNNAFFYY 448

Qy 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISVKRWANFAKYNP 480
Db 449 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISVKRWANFAKYNP 508

Qy 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDEAE 540
Db 509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDEAE 568

Qy 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574
Db 569 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 602
```

RESULT 3
ADRO1039
ID ADRO1039 standard; protein; 574 AA.
XX
AC ADRO1039;

XX 23-SEP-2004 (first entry)
XX Human butyrylcholinesterase A328W/V331L variant.
XX butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addition; human; butyrylcholinesterase variant.
XX Homo sapiens.
OS Synthetic.
OS
XX US2004121970-A1.
XX 24-JUN-2004.
XX 20-DEC-2002; 2002US-00324466.
XX 20-DEC-2002; 2002US-00324466.
XX (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
XX Watkins JD, Pancook JD;
XX WPI; 2004-468195/44.
DR N-PSDB; ADR01038.
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX Claim 1; SEQ ID NO 6; 131pp; English.
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX Sequence 574 AA;
XX Query Match 99.9%; Score 3107; DB 8; Length 574;
XX Best Local Similarity 99.8%; Pred. No. 4.4e-278;
XX Matches 573; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDDIIATNGKVRGMNLTVEGTVTAFLGIPYAPPLGRLEFRFKKPSQSLTKWSDIWNATK 60
Db 1 EDDIIATNGKVRGMNLTVEGTVTAFLGIPYAPPLGRLEFRFKKPSQSLTKWSDIWNATK 60
Qy 61 YANSCCNIDQSPFGHSGEMWNPNTLSEDCLYLNWIPAPKPKNATVLIWYGGGFQT 120
Db 61 YANSCCNIDQSPFGHSGEMWNPNTLSEDCLYLNWIPAPKPKNATVLIWYGGGFQT 120
Qy 121 GTSSLHVYDGFKLARVERVIVVMYRNVGALGFLALPCNPEAPGNMGLFDQQLALQWVQK 180
Db 121 GTSSLHVYDGFKLARVERVIVVMYRNVGALGFLALPCNPEAPGNMGLFDQQLALQWVQK 180
Qy 181 NIAAFGPNKSVTLFPGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGPNKSVTLFPGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Qy 241 NRTNLAKLTGCSRENETETIKLRNKDPOETLLNEAFVVPYGVPTSLVNFPGTVDGDEFLT 300
Db 241 NRTNLAKLTGCSRENETETIKLRNKDPOETLLNEAFVVPYGVPTSLVNFPGTVDGDEFLT 300

Qy 301 DMPDILLELGQFKTKTQILVGVNKDEGTWFLVYGAPGFSKDNNSITTRKEFQEGLKIFPPG 360
Db 301 DMPDILLELGQFKTKTQILVGVNKDEGTWFLVYGAPGFSKDNNSITTRKEFQEGLKIFPPG 360
Qy 361 VSEFGKSIILPHYTDWVDDQRPENYREALGDVGVGDNFICPALBFTKKFSEWGNNAFFY 420
Db 361 VSEFGKSIILPHYTDWVDDQRPENYREALGDVGVGDNFICPALBFTKKFSEWGNNAFFY 420
Qy 421 FEHRSSKLPPEWGMVGHGIEIEFVGLPLERRRDNNTKAEIILSRISIVKRWANFAKYNP 480
Db 421 FEHRSSKLPPEWGMVGHGIEIEFVGLPLERRRDNNTKAEIILSRISIVKRWANFAKYNP 480
Qy 481 NETQNNSTSWPVFKSTQKYLTLNTESTRIMTKLRAOQCRFWTSFFPKVLEMTGNIDAE 540
Db 481 NETQNNSTSWPVFKSTQKYLTLNTESTRIMTKLRAOQCRFWTSFFPKVLEMTGNIDAE 540
Qy 541 WEWKAGFHRNNYNNMDKNOFNNDYTSKKESCVGL 574
Db 541 WEWKAGFHRNNYNNMDKNOFNNDYTSKKESCVGL 574
RESULT 4
ADRO1047
ID ADR01047 standard; protein; 574 AA.
XX AC ADR01047;
XX 23-SEP-2004 (first entry)
XX Human butyrylcholinesterase A328W/S287G/A199S variant.
DE butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addition; human; butyrylcholinesterase variant.
XX Homo sapiens.
OS Synthetic.
XX US2004121970-A1.
XX 24-JUN-2004.
XX 20-DEC-2002; 2002US-00324466.
XX 20-DEC-2002; 2002US-00324466.
XX (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
XX Watkins JD, Pancook JD;
PI WPI; 2004-468195/44.
XX N-PSDB; ADR01046.
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX Claim 1; SEQ ID NO 14; 131pp; English.
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human

```
CC butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;

Query Match          99.8%; Score 3103; DB 8; Length 574;
Best Local Similarity 99.7%; Pred. No. 1e-277;
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGGTTAFGLGIPYAQPPLGRGRFKKPSQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFGGTTAFGLGIPYAQPPLGRGRFKKPSQSLTKWSDIWNATK 60

QY 61 YANSCCNIDQSFPGFHGSEMNPNITLSEDCLYLNWIPAPKPKNATVLIWIYGGGFOT 120
DB 61 YANSCCNIDQSFPGFHGSEMNPNITLSEDCLYLNWIPAPKPKNATVLIWIYGGGFOT 120

QY 121 GTSSLHVYDGFKLARVERVIVSMNRYVAGLFGFLALPGNPAAGNMGFLDQQLALQWVQK 180
DB 121 GTSSLHVYDGFKLARVERVIVSMNRYVAGLFGFLALPGNPAAGNMGFLDQQLALQWVQK 180

QY 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTLNLAKLTCGSRNETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
DB 241 NRTLNLAKLTCGSRNETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

QY 241 NRTLNLAKLTCGSRNETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
DB 241 NRTLNLAKLTCGSRNETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

QY 301 DMPDILLBLGQFKTKTQILVGNVKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
DB 301 DMPDILLBLGQFKTKTQILVGNVKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYDNFICPALEFTKKFSEWGNNAFFYY 420
DB 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYDNFICPALEFTKKFSEWGNNAFFYY 420

QY 421 FEHRSSKLPWPPEWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISIVKRWANFAYKGNP 480
DB 421 FEHRSSKLPWPPEWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISIVKRWANFAYKGNP 480

QY 481 NETQNNSTSWPVFKSTEOKYLTLTNTESTRIMTKLRAQOCRFWTSFFPKVLEMTGNIDEAE 540
DB 481 NETQNNSTSWPVFKSTEOKYLTLTNTESTRIMTKLRAQOCRFWTSFFPKVLEMTGNIDEAE 540

QY 541 WEWKAGFHRWNNYMDWKNQFNDYTSKESCVGL 574
DB 541 WEWKAGFHRWNNYMDWKNQFNDYTSKESCVGL 574

RESULT 5
ADRO1051
ID ADRO1051 standard; protein; 574 AA.
XX
AC ADRO1051;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/F227A variant.
XX
KW butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.

XX (WATK/) WATKINS J D.
XX (PANC/) PANCOOK J D.
XX
XX Watkins JD, Pancook JD;
XX WPI; 2004-468195/44.
XX N-PSDB; ADR01050.
XX
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine
XX -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
XX Claim 1; SEQ ID NO 18; 131pp; English.
XX
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
XX comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
XX NOS: 2-42) or their functional fragments. Also described are: a nucleic
XX acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
XX bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
XX cocaine-induced condition; and a method of hydrolysing a cocaine-based
XX butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
XX polypeptide comprising any of the 21 sequences of 57 amino acids each
XX (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
XX 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
XX butyrylcholinesterase variant polypeptides and nucleic acids and methods
XX are useful in treating cocaine-induced condition i.e. cocaine-overdose or
XX cocaine addiction. This is the amino acid sequence of a human
XX butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;

Query Match          99.7%; Score 3102; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.3e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGGTTAFGLGIPYAQPPLGRGRFKKPSQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFGGTTAFGLGIPYAQPPLGRGRFKKPSQSLTKWSDIWNATK 60

QY 61 YANSCCNIDQSFPGFHGSEMNPNITLSEDCLYLNWIPAPKPKNATVLIWIYGGGFOT 120
DB 61 YANSCCNIDQSFPGFHGSEMNPNITLSEDCLYLNWIPAPKPKNATVLIWIYGGGFOT 120

QY 121 GTSSLHVYDGFKLARVERVIVSMNRYVAGLFGFLALPGNPAAGNMGFLDQQLALQWVQK 180
DB 121 GTSSLHVYDGFKLARVERVIVSMNRYVAGLFGFLALPGNPAAGNMGFLDQQLALQWVQK 180

QY 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTLNLAKLTCGSRNETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
DB 241 NRTLNLAKLTCGSRNETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

QY 301 DMPDILLBLGQFKTKTQILVGNVKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
DB 301 DMPDILLBLGQFKTKTQILVGNVKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYDNFICPALEFTKKFSEWGNNAFFYY 420
DB 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYDNFICPALEFTKKFSEWGNNAFFYY 420

QY 421 FEHRSSKLPWPPEWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISIVKRWANFAYKGNP 480
DB 421 FEHRSSKLPWPPEWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISIVKRWANFAYKGNP 480

QY 481 NETQNNSTSWPVFKSTEOKYLTLTNTESTRIMTKLRAQOCRFWTSFFPKVLEMTGNIDEAE 540
DB 481 NETQNNSTSWPVFKSTEOKYLTLTNTESTRIMTKLRAQOCRFWTSFFPKVLEMTGNIDEAE 540

QY 541 WEWKAGFHRWNNYMDWKNQFNDYTSKESCVGL 574
DB 541 WEWKAGFHRWNNYMDWKNQFNDYTSKESCVGL 574
```


Db 541 WEWKAGFHRNNYMDWKNQFNNDYTSKESCVGL 574

RESULT 6
ADRO1035
ID ADRO1035 standard; protein; 574 AA.
XX
AC ADRO1035;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/Y332M variant.
XX
KW butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addition; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.
XX
PA (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
XX
PI Watkins JD, Pancook JD;
XX
DR WPI; 2004-468195/44.
DR N-PSDB; ADRO1034.
XX
PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
PS Claim 1; SEQ ID NO 2; 131pp; English.
XX
CC The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolyzing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;
Query Match 99.7%; Score 3102; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.3e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDDIIATKNGKVRGNLTVFGGTAFGLGIPYAPPLGRLFKKFQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGNLTVFGGTAFGLGIPYAPPLGRLFKKFQSLTKWSDIWNATK 60
QY 61 YANSCQNDIQSFPGHSGEMNPNLTDSEDCLYLNWVIPAPKPNATVLIWYGGGQT 120
Db 61 YANSCQNDIQSFPGHSGEMNPNLTDSEDCLYLNWVIPAPKPNATVLIWYGGGQT 120
QY 121 GTSSLHVYDGKFLARVERIVVSMRYVGMVYVGVNGLFALPGNPEAPGNGLFDQOLALQWQK 180
Db 121 GTSSLHVYDGKFLARVERIVVSMRYVGMVYVGVNGLFALPGNPEAPGNGLFDQOLALQWQK 180

QY 181 NIAAFGGNPKSVTLFGSGAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGSGAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
QY 241 NRTNLAKLTGCSRENETEIIKCLRNKDPQELLNEAFVVPVGTPLSVNFGPTVDDGDLT 300
Db 241 NRTNLAKLTGCSRENETEIIKCLRNKDPQELLNEAFVVPVGTPLSVNFGPTVDDGDLT 300
QY 301 DMPDILLELGQFKTKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 360
Db 301 DMPDILLELGQFKTKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 360
QY 361 VSEFGKESILFHYTDVDDQRPENYREALGVGDYDNFICPALETKKFSWGNNAFFYY 420
Db 361 VSEFGKESILFHYTDVDDQRPENYREALGVGDYDNFICPALETKKFSWGNNAFFYY 420
QY 421 FEHRSSKLPWPEWGMVHGIEFVFGPLPERRDNYTKAEILLRSIVKRWANFAKYNP 480
Db 421 FEHRSSKLPWPEWGMVHGIEFVFGPLPERRDNYTKAEILLRSIVKRWANFAKYNP 480
QY 481 NETQNNSTSWPVFKSTEOKYLTNTTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540
Db 481 NETQNNSTSWPVFKSTEOKYLTNTTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540
QY 541 WEWKAGFHRNNYMDWKNQFNNDYTSKESCVGL 574
Db 541 WEWKAGFHRNNYMDWKNQFNNDYTSKESCVGL 574

RESULT 7
ADRO1041
ID ADRO1041 standard; protein; 574 AA.
XX
AC ADRO1041;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/Y332S variant.
XX
KW butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addition; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.
XX
PA (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
XX
PI Watkins JD, Pancook JD;
XX
DR WPI; 2004-468195/44.
DR N-PSDB; ADRO1040.
XX
PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
PS Claim 1; SEQ ID NO 8; 131pp; English.
XX
CC The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolyzing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;
Query Match 99.7%; Score 3102; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.3e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDDIIATKNGKVRGNLTVFGGTAFGLGIPYAPPLGRLFKKFQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGNLTVFGGTAFGLGIPYAPPLGRLFKKFQSLTKWSDIWNATK 60
QY 61 YANSCQNDIQSFPGHSGEMNPNLTDSEDCLYLNWVIPAPKPNATVLIWYGGGQT 120
Db 61 YANSCQNDIQSFPGHSGEMNPNLTDSEDCLYLNWVIPAPKPNATVLIWYGGGQT 120
QY 121 GTSSLHVYDGKFLARVERIVVSMRYVGMVYVGVNGLFALPGNPEAPGNGLFDQOLALQWQK 180
Db 121 GTSSLHVYDGKFLARVERIVVSMRYVGMVYVGVNGLFALPGNPEAPGNGLFDQOLALQWQK 180

CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
XX Sequence 574 AA;

Query Match 99.7%; Score 3101; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.6e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFSGTATFLGIPYAQPPLGRURFKKPSQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFSGTATFLGIPYAQPPLGRURFKKPSQSLTKWSDIWNATK 60

QY 61 YANSCCQNIQSFPGFHGSEMNPNLTDSEDCLYLNWIWIPAPKPKNATVLIWYGGGFQT 120
DB 61 YANSCCQNIQSFPGFHGSEMNPNLTDSEDCLYLNWIWIPAPKPKNATVLIWYGGGFQT 120

QY 121 GTSSLVHYDGFARVERVIVSMNRYVGLGFLALPGNPEAPGNMGLFDQQLALQWVQK 180
DB 121 GTSSLVHYDGFARVERVIVSMNRYVGLGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

QY 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGPPLSVNFGPTVDGDFLT 300
DB 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGPPLSVNFGPTVDGDFLT 300

QY 301 DMPDILLELQGFKKTQILVGVNKGDEGTWFLVYGAFGFSKNNNSIITRKEFOEGLKIFPPG 360
DB 301 DMPDILLELQGFKKTQILVGVNKGDEGTWFLVYGAFGFSKNNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDGYNFICPALEFTKKFSEWGNAPFFY 420
DB 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDGYNFICPALEFTKKFSEWGNAPFFY 420

QY 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKABEILSRIKRWANFAKYNP 480
DB 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKABEILSRIKRWANFAKYNP 480

QY 481 NETQNNSTSWPVFKSTEOKYLTLTNTESTRIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 540
DB 481 NETQNNSTSWPVFKSTEOKYLTLTNTESTRIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 540

QY 541 WEWKAGFHRNNYMDWQNDYTSKESCVGL 574
DB 541 WEWKAGFHRNNYMDWQNDYTSKESCVGL 574

RESULT 8

ADRO1037
ID ADRO1037 standard; protein; 574 AA.
XX
AC ADRO1037;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/Y332P variant.
XX
DE butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.

XX US2004121970-A1.
PN 24-JUN-2004.
PD
XX 20-DEC-2002; 2002US-00324466.
PF
XX 20-DEC-2002; 2002US-00324466.
PR
XX (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
FA
XX Watkins JD, Pancook JD;
PI
XX WPI: 2004-468195/44.
DR N-PSDB; ADR01036.
XX
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
XX Claim 1; SEQ ID NO 4; 131pp; English.
XX
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
XX Sequence 574 AA;

Query Match 99.7%; Score 3100; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 2e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFSGTATFLGIPYAQPPLGRURFKKPSQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFSGTATFLGIPYAQPPLGRURFKKPSQSLTKWSDIWNATK 60

QY 61 YANSCCQNIQSFPGFHGSEMNPNLTDSEDCLYLNWIWIPAPKPKNATVLIWYGGGFQT 120
DB 61 YANSCCQNIQSFPGFHGSEMNPNLTDSEDCLYLNWIWIPAPKPKNATVLIWYGGGFQT 120

QY 121 GTSSLVHYDGFARVERVIVSMNRYVGLGFLALPGNPEAPGNMGLFDQQLALQWVQK 180
DB 121 GTSSLVHYDGFARVERVIVSMNRYVGLGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

QY 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGPPLSVNFGPTVDGDFLT 300
DB 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGPPLSVNFGPTVDGDFLT 300

QY 301 DMPDILLELQGFKKTQILVGVNKGDEGTWFLVYGAFGFSKNNNSIITRKEFOEGLKIFPPG 360
DB 301 DMPDILLELQGFKKTQILVGVNKGDEGTWFLVYGAFGFSKNNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDGYNFICPALEFTKKFSEWGNAPFFY 420
DB 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDGYNFICPALEFTKKFSEWGNAPFFY 420

QY 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKABEILSRIKRWANFAKYNP 480
DB 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKABEILSRIKRWANFAKYNP 480

Db 421 FEHRSSKLPWPEWGMVGHGIEFVFGLEPLERRDNYTKAEILSRISIVKRWANFAKYGNP 480
QY 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAE 540
QY 541 WEWKAGFHRWNNYMDWKQNFNDYTSKKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKQNFNDYTSKKESCVGL 574

RESULT 9
AAO18944
ID AAO18944 standard; protein; 574 AA.
XX
XX AAO18944;
DT 02-DEC-2002 (first entry)
XX Human butyrylcholinesterase mutant A328W.
DE Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
KW cocaine addition; antidiabetic; antidote; mutein.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 328
FT /note= "wild-type Ala substituted by Trp"
XX
XX WO200264796-A2.
XX
XX 22-AUG-2002.
XX
XX 21-DEC-2001; 2001WO-US050450.
XX
XX 26-DEC-2000; 2000US-00748739.
PR 20-DEC-2001; 2001US-00032233.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
PA (UYNE-) UNIV NEBRASKA MEDICAL CENT.
XX
XX Lockridge O, Watkins JD, Pancook JD;
PI
XX
XX WPI; 2002-636633/68.
DR
XX
XX New human butyrylcholinesterase variant polypeptides, useful for treating
PT cocaine-induced conditions.
XX
XX Example 1; Page; 150pp; English.
XX
XX The present invention relates to mutants of human butyrylcholinesterase.
CC The enzymes have an increased cocaine hydrolysis activity and can be used
CC for treating a cocaine-induced condition. The present sequence is a
CC mutant protein shown in the exemplification of the invention
XX
XX Sequence 574 AA;
SQ

Query Match 99.6%; Score 3099; DB 5; Length 574;
Best Local Similarity 99.8%; Pred. No. 2.4e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGNLTVFGSTVTAFLGIPYAOPLGLRFRFKKQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGNLTVFGSTVTAFLGIPYAOPLGLRFRFKKQSLTKWSDIWNATK 60
QY 61 YANSCQNIQDSFPGHSEMMNPNTDLSDECLYNVWIPAPKPNATVLIWYGGGQT 120
Db 61 YANSCQNIQDSFPGHSEMMNPNTDLSDECLYNVWIPAPKPNATVLIWYGGGQT 120
QY 121 GTSSLHVVDGKFLARVERVIVVMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 180

Db 121 GTSSLHVVDGKFLARVERVIVVMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 180
QY 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
QY 241 NRTLLAKLTGCSRENETEIIKCLRNKDPQELLNEAFVVPYGTPLSVNFGTVDGDFLT 300
Db 241 NRTLLAKLTGCSRENETEIIKCLRNKDPQELLNEAFVVPYGTPLSVNFGTVDGDFLT 300
QY 301 DMPDILLELGOFKKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFOEGKIFPPG 360
Db 301 DMPDILLELGOFKKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFOEGKIFPPG 360
QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYFNFCIPALEFTKKFSEGNNAFFYY 420
Db 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYFNFCIPALEFTKKFSEGNNAFFYY 420
QY 421 FEHRSSKLPWPEWGMVGHGIEFVFGLEPLERRDNYTKAEILSRISIVKRWANFAKYGNP 480
Db 421 FEHRSSKLPWPEWGMVGHGIEFVFGLEPLERRDNYTKAEILSRISIVKRWANFAKYGNP 480
QY 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAE 540
QY 541 WEWKAGFHRWNNYMDWKQNFNDYTSKKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKQNFNDYTSKKESCVGL 574

RESULT 10
ADRO1049
ID ADRO1049 standard; protein; 574 AA.
XX
XX AC ADRO1049;
XX
XX 23-SEP-2004 (first entry)
XX Human butyrylcholinesterase A328W/S287G/P227A variant.
XX
XX butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX US2004121970-A1.
PN
XX
XX 24-JUN-2004.
PD
XX
XX 20-DEC-2002; 2002US-00324466.
PF
XX
XX 20-DEC-2002; 2002US-00324466.
PR
XX
XX (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
XX
XX Watkins JD, Pancook JD;
PI
XX WPI; 2004-468195/44.
XX
XX N-PSDB; ADRO1048.
DR
XX
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
PT
XX
XX Claim 1; SEQ ID NO 16; 131pp; English.
PS
XX
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416

CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (1) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
XX
SQ Sequence 574 AA;

Query Match 99.6%; Score 3098; DB 8; Length 574;
Best Local Similarity 99.7%; Pred. No. 3e-277;
Matches 572; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EDDIIATKNGKVRGMNLTVEGGTVTAFLGIPYAQPPLGRGRFKKPSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGMNLTVEGGTVTAFLGIPYAQPPLGRGRFKKPSLTKWSDIWNATK 60
Qy 61 YANSCCNIDQSPFGFHGSEMNPNTDLSBCLYLNVMIPAPKPNATVLIWIYGGGQFT 120
Db 61 YANSCCNIDQSPFGFHGSEMNPNTDLSBCLYLNVMIPAPKPNATVLIWIYGGGQFT 120
Qy 121 GTSSHYVDGKFLARVERVIVSNRYVGALGFLALPCNPEAPGNMGLFDQOLALQWVK 180
Db 121 GTSSHYVDGKFLARVERVIVSNRYVGALGFLALPCNPEAPGNMGLFDQOLALQWVK 180
Qy 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRALQSGSANAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRALQSGSANAPWAVTSLYEAR 240
Qy 241 NRTNLAKLTGCSRENETEIIKCLRNDQDQOILNEAPVVPYGPPLSVNGFPTVDGDFLT 300
Db 241 NRTNLAKLTGCSRENETEIIKCLRNDQDQOILNEAPVVPYGPPLSVNGFPTVDGDFLT 300
Qy 301 DMPDILLELGQFKKTQILVGNKDEGTWFLVYGAPGFSKONNSIITRKEFOEGLKIFPPG 360
Db 301 DMPDILLELGQFKKTQILVGNKDEGTWFLVYGAPGFSKONNSIITRKEFOEGLKIFPPG 360
Qy 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYDYNFICPALEFTKKFSEWGNNAFFY 420
Db 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYDYNFICPALEFTKKFSEWGNNAFFY 420
Qy 421 FEHRSSKLPPPEWGMVHGIEFVFGPLPLRRDNYTKAEIILSRISIVKRWANFAKYNP 480
Db 421 FEHRSSKLPPPEWGMVHGIEFVFGPLPLRRDNYTKAEIILSRISIVKRWANFAKYNP 480
Qy 481 NETQNNSTWPFVKSTEQKYLTLTNTSTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAE 540
Db 481 NETQNNSTWPFVKSTEQKYLTLTNTSTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAE 540
Qy 541 WEWKAGFHRMNNYMDWKNQFNNDYTSKESCVGL 574
Db 541 WEWKAGFHRMNNYMDWKNQFNNDYTSKESCVGL 574

RESULT 11
AAE25235
XX AAE25235 standard; protein; 574 AA.
XX
AC AAE25235;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human butyrylcholinesterase protein.
XX
XX Human; optimisation; drug; butyrylcholinesterase; enzyme.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers

FT Disulfide-bond 65..92
FT Region 68..82
FT /note= "Region used to generate focussed libraries"
FT Active-site 82
FT /note= "Aromatic active site gorge residue"
FT Region 110..121
FT /note= "Region used to generate focussed libraries"
FT Active-site 112
FT /note= "Aromatic active site gorge residue"
FT Active-site 128
FT /note= "Aromatic active site gorge residue"
FT Region 194..201
FT /note= "Region used to generate focussed libraries"
FT Region 224..234
FT /note= "Region used to generate focussed libraries"
FT Active-site 231
FT /note= "Aromatic active site gorge residue"
FT Disulfide-bond 252..263
FT Region 277..289
FT /note= "Region used to generate focussed libraries"
FT Region 327..332
FT /note= "Region used to generate focussed libraries"
FT Active-site 329
FT /note= "Aromatic active site gorge residue"
FT Active-site 332
FT /note= "Aromatic active site gorge residue"
FT Disulfide-bond 400..519
FT Region 429..442
FT /note= "Region used to generate focussed libraries"
FT Active-site 430
FT /note= "Aromatic active site gorge residue"
FT Active-site 440
FT /note= "Aromatic active site gorge residue"
XX
XX W020024361-A2.
PN
XX
XX 06-JUN-2002.
PD
XX
XX 28-NOV-2001; 2001WO-US044600.
PF
XX
XX 28-NOV-2000; 2000US-00724762.
PR
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
PA
XX
XX Huse WD;
PI
XX
XX WPT; 2002-519586/55.
DR
XX
XX New cell composition having population of non-yeast eukaryotic cells
PT containing diverse population of variant nucleic acids that are expressed
PT in different cell and located within each cell at identical site in
PT genome.
XX
XX Example 11; Page 155-156; 157pp; English.
PS
XX
XX The present invention relates to a cell composition having population of
CC non-yeast eukaryotic cells containing a diverse population of ten or more
CC variant nucleic acids or heterologous nucleic acid fragments comprising
CC distinct species of nucleic acid fragments, each of the variant nucleic
CC acids or heterologous nucleic acid fragments being expressed in different
CC cells and located within each cell at an identical site in the genome.
CC The composition is useful to identify polypeptides exhibiting optimised
CC activity. It is also useful for identifying a binding ligand. It is also
CC useful for identifying specific ligands to desired target molecules. Such
CC ligands can be developed as potential drug candidates or alternatively
CC used as lead compounds for the generation and identification of ligand
CC variants which exhibit enhanced activity of the desired binding property.
CC The methods can similarly be applied to identify a nucleic acid having an
CC optimised activity by screening for an activity associated with a parent
CC nucleic acid. The present sequence is human butyrylcholinesterase
CC protein. This sequence is used in the exemplification of the invention
XX
XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.6e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVEGTTAFGLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVEGTTAFGLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60

QY 61 YANSCCQNIQDQFPFGHSEMMNPNTDSECLYLNVMIPAPKPKNATVLIWIYGGGQT 120
DB 61 YANSCCQNIQDQFPFGHSEMMNPNTDSECLYLNVMIPAPKPKNATVLIWIYGGGQT 120

QY 121 GTSSLHVVDGKFLARVERVIVSMNRYVGAFLALPGNPEAPGNMGLFDQQLALQWVOK 180
DB 121 GTSSLHVVDGKFLARVERVIVSMNRYVGAFLALPGNPEAPGNMGLFDQQLALQWVOK 180

QY 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTLNKLATGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
DB 241 NRTLNKLATGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

QY 301 DMPDILLLELQPKTKTQILVGVNKGDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360
DB 301 DMPDILLLELQPKTKTQILVGVNKGDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFKESILPHYTDWDDQRPENYREALGDVVDYNTFCPALEFTKKPSEWGNNAFFY 420
DB 361 VSEFKESILPHYTDWDDQRPENYREALGDVVDYNTFCPALEFTKKPSEWGNNAFFY 420

QY 421 FEHRSSKLPWPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
DB 421 FEHRSSKLPWPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISIVKRWANFAKYGNP 480

QY 481 NETQNNSTSWPVFKSTEOKYLTNTSTRTIMTKLRAOQCRFTWSPFPKVLMTGNIDAE 540
DB 481 NETQNNSTSWPVFKSTEOKYLTNTSTRTIMTKLRAOQCRFTWSPFPKVLMTGNIDAE 540

QY 541 WEWKAGFHRWNNYMDWKNQNDYTSKESCVGL 574
DB 541 WEWKAGFHRWNNYMDWKNQNDYTSKESCVGL 574

RESULT 12

AAO18982
ID AAO18982 standard; protein; 574 AA.

XX AC AAO18982;

XX DT 02-DEC-2002 (first entry)

XX DE Human butyrylcholinesterase mutant A328/V331L.

XX KW Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
XX KW cocaine addition; antiaddictive; antidote; muten.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 328

FT /note= "wild-type Ala substituted by Trp"

FT Misc-difference 331

FT /note= "wild-type Val substituted by Leu"

XX WO200264796-A2.

XX PD 22-AUG-2002.

XX PF 21-DEC-2001; 2001WO-US050450.

XX 26-DEC-2000; 2000US-00748739.
PR 20-DEC-2001; 2001US-00032233.
XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX (UYNE-) UNIV NEBRASKA MEDICAL CENT.
PI Lockridge O, Watkins JD, Pancook JD;
XX WPI; 2002-636633/68.
XX New human butyrylcholinesterase variant polypeptides, useful for treating
PT cocaine-induced conditions.
XX Claim 1; Page; 150pp; English.
XX The present invention relates to mutants of human butyrylcholinesterase.
CC The enzymes have an increased cocaine hydrolysis activity and can be used
CC for treating a cocaine-induced condition. The present sequence is a
CC mutant protein shown in the exemplification of the invention
XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;

Best Local Similarity 99.7%; Pred. No. 4.6e-277;

Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVEGTTAFGLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60

DB 1 EDDIIATKNGKVRGMNLTVEGTTAFGLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60

QY 61 YANSCCQNIQDQFPFGHSEMMNPNTDSECLYLNVMIPAPKPKNATVLIWIYGGGQT 120

DB 61 YANSCCQNIQDQFPFGHSEMMNPNTDSECLYLNVMIPAPKPKNATVLIWIYGGGQT 120

QY 121 GTSSLHVVDGKFLARVERVIVSMNRYVGAFLALPGNPEAPGNMGLFDQQLALQWVOK 180

DB 121 GTSSLHVVDGKFLARVERVIVSMNRYVGAFLALPGNPEAPGNMGLFDQQLALQWVOK 180

QY 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

DB 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTLNKLATGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

DB 241 NRTLNKLATGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

QY 301 DMPDILLLELQPKTKTQILVGVNKGDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360

DB 301 DMPDILLLELQPKTKTQILVGVNKGDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFKESILPHYTDWDDQRPENYREALGDVVDYNTFCPALEFTKKPSEWGNNAFFY 420

DB 361 VSEFKESILPHYTDWDDQRPENYREALGDVVDYNTFCPALEFTKKPSEWGNNAFFY 420

QY 421 FEHRSSKLPWPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISIVKRWANFAKYGNP 480

DB 421 FEHRSSKLPWPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISIVKRWANFAKYGNP 480

QY 481 NETQNNSTSWPVFKSTEOKYLTNTSTRTIMTKLRAOQCRFTWSPFPKVLMTGNIDAE 540

DB 481 NETQNNSTSWPVFKSTEOKYLTNTSTRTIMTKLRAOQCRFTWSPFPKVLMTGNIDAE 540

QY 541 WEWKAGFHRWNNYMDWKNQNDYTSKESCVGL 574

DB 541 WEWKAGFHRWNNYMDWKNQNDYTSKESCVGL 574

RESULT 13

AAO18898

ID AAO18898 standard; protein; 574 AA.

XX AC AAO18898;

XX 02-DEC-2002 (first entry)
DT Human butyrylcholinesterase.
XX
DE Human butyrylcholinesterase.
XX
XX Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
KW cocaine addiction; antiaddictive; antidote.
XX
KW Homo sapiens.
OS
XX WO200264796-A2.
XX
XX 22-AUG-2002.
XX
XX 21-DEC-2001; 2001WO-US050450.
XX
XX 26-DEC-2000; 2000US-00748739.
PR
XX 20-DEC-2001; 2001US-00032233.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
PA (UYNE-) UNIV NEBRASKA MEDICAL CENT.
XX
XX Lockridge O, Watkins JD, Pancook JD;
XX
XX WPI; 2002-636633/68.
XX
XX New human butyrylcholinesterase variant polypeptides, useful for treating
PT cocaine-induced conditions.
XX
XX Example 3; Fig 2; 150pp; English.
XX
XX The present invention relates to mutants of human butyrylcholinesterase.
CC The enzymes have an increased cocaine hydrolysis activity and can be used
CC for treating a cocaine-induced condition. The present sequence is a
CC protein shown in the exemplification of the invention
XX
SQ Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.6e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAQPPLGRFRFKKPSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAQPPLGRFRFKKPSLTKWSDIWNATK 60

Qy 61 YANSCCQIDQSPFGFHGSEMMNPNTDLSBCLYLNWVWPAPKPNATVLIWIYGGGFQT 120
Db 61 YANSCCQIDQSPFGFHGSEMMNPNTDLSBCLYLNWVWPAPKPNATVLIWIYGGGFQT 120

Qy 121 GTSSLHYVDGKFLARVERVIVSMNYRVGALGFLALPGNPEAPGNMGLFDQOLALQWVQK 180
Db 121 GTSSLHYVDGKFLARVERVIVSMNYRVGALGFLALPGNPEAPGNMGLFDQOLALQWVQK 180

Qy 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSNFAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSNFAPWAVTSLYEAR 240

Qy 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGTPLSVNFGTVDGDFLT 300
Db 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGTPLSVNFGTVDGDFLT 300

Qy 301 DMPDILLBELGOFKKTQIILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPG 360
Db 301 DMPDILLBELGOFKKTQIILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPG 360

Qy 361 VSEFGKESILFHYTDVDDQRPENYREALGDVVDYNEICPALFTFKFSEWGNNAFFY 420
Db 361 VSEFGKESILFHYTDVDDQRPENYREALGDVVDYNEICPALFTFKFSEWGNNAFFY 420

Qy 421 FEHRSSKLPWPEWGMVHGYSIEIFVFGPLPERRDNYTKAEIILSRIVKRWANFAKYNP 480
Db 421 FEHRSSKLPWPEWGMVHGYSIEIFVFGPLPERRDNYTKAEIILSRIVKRWANFAKYNP 480

Qy 481 NETONNSTSWPKSTEQKYLTLNTSTRTIMTKLRAOQCRFWTSFPPKVLMTGNIDEAE 540
Db 481 NETONNSTSWPKSTEQKYLTLNTSTRTIMTKLRAOQCRFWTSFPPKVLMTGNIDEAE 540

Qy 541 WEWKAGFHRWNNYMMDMKQNFNDYTSKKESCUGL 574
Db 541 WEWKAGFHRWNNYMMDMKQNFNDYTSKKESCUGL 574

RESULT 14

ABR62391
ID ABR62391 standard; protein; 574 AA.

XX ABR62391;

XX 03-OCT-2003 (first entry)

XX Human butyrylcholinesterase.

XX Human; butyrylcholinesterase; transgenic; poisoning; antidote; enzyme;
KW EC-3.1.1.8.

XX Homo sapiens.

XX WO2003054182-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-IB005526.

XX 21-DEC-2001; 2001US-0344295P.

XX (NEXI-) NEXIA BIOTECHNOLOGIES INC.

XX Karatzas C, Huang Y, Lazaris A;

XX WPI; 2003-559148/52.

XX N-PSDB; ACC84169.

XX New transgenic mammal (e.g. goat) expressing a butyrylcholinesterase
(BChE) enzyme in its milk or urine, useful for large-scale production of
PT recombinant BChE to prevent or treat organophosphate poisoning or cocaine
PT intoxication.

XX Claim 10; Page 100-102; 112pp; English.

XX The present sequence is the protein sequence of human
CC butyrylcholinesterase (BChE). The invention provides methods for large-
CC scale production of recombinant BChE in cell culture, and in the milk
CC and/or urine of transgenic mammals. The genome of the transgenic mammal
CC (e.g. goat) comprises a DNA sequence that encodes BChE operably linked to
CC a mammary gland-specific promoter or to a urinary endothelium-specific
CC promoter, and a signal sequence that provides secretion of the BChE
CC enzyme into the milk or urine of the mammal. The recombinant BChE can be
CC used in preventing and/or treating organophosphate pesticide poisoning,
CC nerve gas poisoning, cocaine intoxication or succinylcholine-induced
CC apnoea

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 6; Length 574;

Best Local Similarity 99.8%; Pred. No. 4.6e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAQPPLGRFRFKKPSLTKWSDIWNATK 60

Db 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAQPPLGRFRFKKPSLTKWSDIWNATK 60

Qy 61 YANSCCQIDQSPFGFHGSEMMNPNTDLSBCLYLNWVWPAPKPNATVLIWIYGGGFQT 120

Db 61 YANSCCQIDQSPFGFHGSEMMNPNTDLSBCLYLNWVWPAPKPNATVLIWIYGGGFQT 120

```
QY 121 GTSSLLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVK 180
Db 121 GTSSLLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVK 180
QY 181 NIAAFGCGNPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGCGNPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
QY 241 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVGDGFLT 300
Db 241 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVGDGFLT 300
QY 301 DMPDILLLELGQKKTQIILGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFQSGLKIFPPG 360
Db 301 DMPDILLLELGQKKTQIILGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFQSGLKIFPPG 360
QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEGNNAFFY 420
Db 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEGNNAFFY 420
QY 421 FEHRSSKLPWPPEWGMVHGIEFVFGFLPERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
Db 421 FEHRSSKLPWPPEWGMVHGIEFVFGFLPERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
QY 481 NETQNNSTSWPVKSTEQKYLTLNTESTIMTKLRAQQCRFWTSPPPKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVKSTEQKYLTLNTESTIMTKLRAQQCRFWTSPPPKVLEMTGNIDEAE 540
QY 541 WEWKAGFHRWNNYMDKQNDYTSKESCVGL 574
Db 541 WEWKAGFHRWNNYMDKQNDYTSKESCVGL 574

RESULT 15
ID ABW00695 standard; protein; 574 AA.
AC ABW00695;
XX
XX
DT 15-JAN-2004 (first entry)
XX
DE Human butyrylcholinesterase protein.
XX
KW Human; butyrylcholinesterase; enzyme.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT 68..82 Location/Qualifiers
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase"
FT 82
FT Active-site
FT Region
FT 110..121
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase variants"
FT 112
FT Active-site
FT Active-site
FT Region
FT 128
FT 194..201
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase"
FT 224..234
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase variants"
FT 231
FT Active-site
FT Region
FT 277..289
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase variants"
FT 327..332
FT Region
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase"
FT 329
FT Active-site
FT Active-site
FT Region
FT 429..442
```

```
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase variants"
FT Active-site
FT Active-site
XX 430
XX 440
XX US2003096401-A1.
XX 22-MAY-2003.
XX 28-NOV-2001; 2001US-00997209.
XX 28-NOV-2000; 2000US-0367370P.
XX (HUSE/) HUSE W D.
XX Huse WD;
XX WPI; 2003-786991/74.
XX
XX Cell composition comprises non-yeast eukaryotic cells having diverse
XX population of variant nucleic acids or heterologous nucleic acid
XX fragments, useful for identifying polypeptide with optimized activity.
XX
XX Example 11; Fig 8; Opp; English.
XX
XX The invention relates to a cell composition comprising a population of
XX non-yeast eukaryotic cells containing diverse population of variant
XX nucleic acids, or heterologous nucleic acid fragments with distinct
XX species of nucleic acid fragments, where each of the variant nucleic
XX acids or heterologous nucleic acid fragments are expressed in different
XX cell and located within each cell at an identical site in the genome. The
XX invention is useful for identifying polypeptide with optimised activity
XX and for identifying a polypeptide receptor for a ligand. The present
XX sequence is human butyrylcholinesterase protein. This sequence is used in
XX the exemplification of the invention
XX
XX Sequence 574 AA;
XX
Query Match 99.5%; Score 3096; DB 7; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.6e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDDIIATKNGKVRGMNLTVFGGTVTAFGLGIPYAPPLGRLFKFKPQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGMNLTVFGGTVTAFGLGIPYAPPLGRLFKFKPQSLTKWSDIWNATK 60
QY 61 YANSCCQNDIOSFPGFHGSEMNPNTDLSDCLYLNWVWPAPKPNATVLIWYGGFOT 120
Db 61 YANSCCQNDIOSFPGFHGSEMNPNTDLSDCLYLNWVWPAPKPNATVLIWYGGFOT 120
QY 121 GTSSLLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVK 180
Db 121 GTSSLLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVK 180
QY 181 NIAAFGCGNPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGCGNPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
QY 241 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVGDGFLT 300
Db 241 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVGDGFLT 300
QY 301 DMPDILLLELGQKKTQIILGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFQSGLKIFPPG 360
Db 301 DMPDILLLELGQKKTQIILGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFQSGLKIFPPG 360
QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEGNNAFFY 420
Db 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEGNNAFFY 420
QY 421 FEHRSSKLPWPPEWGMVHGIEFVFGFLPERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
Db 421 FEHRSSKLPWPPEWGMVHGIEFVFGFLPERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
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Qy 481 NETQNNSTSWPVKSTEQXYLTLTNTSTRIIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 NETQNNSTSWPVKSTEQXYLTLTNTSTRIIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 WEWKAGFHRWNNYMDWKNQFNDYTSKKESCVGL 574
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 WEWKAGFHRWNNYMDWKNQFNDYTSKKESCVGL 574
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: July 8, 2005, 11:12:36
Job time : 80 secs

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OM protein - protein search, using sw model

Run on: July 8, 2005, 11:11:07 ; Search time 71 Seconds
(without alignments)
4139.908 Million cell updates/sec

Title: US-09-748-739a-2_COPY_29_602

Perfect score: 3110

Sequence: 1 EDIIIIATKNGKVRGNLTV.....MDWKQFNIDYTSKESCVGL 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	3096	99.5	602	1	CHLE_HUMAN
2	2843	91.4	581	1	CHLE_RABIT
3	2775	89.2	602	2	Q9N1N9
4	2774	89.2	574	1	CHLE_HORSE
5	2696	86.7	602	1	CHLE_FELCA
6	2684	86.3	602	1	CHLE_PANNTT
7	2521	81.1	603	1	CHLE_MOUSE
8	2505	80.5	597	2	Q9JUK1
9	2289	73.6	603	2	Q90ZK8
10	1765.5	56.8	634	1	ACBS_BRARE
11	1765	56.8	633	1	ACBS_ELEEL
12	1722.5	55.4	606	1	ACBS_BUNFA
13	1691	54.4	614	2	Q67BC1
14	1689	54.3	614	1	ACBS_HUMAN
15	1678.5	54.0	614	1	ACBS_RAT
16	1675.5	53.9	614	1	ACBS_MOUSE
17	1674	53.6	349	2	Q9GKJ6
18	1666.5	53.6	611	1	ACBS_FELCA
19	1663.5	53.5	613	1	ACBS_BOVIN
20	1649.5	53.0	584	1	ACBS_RABIT
21	1649	53.0	590	1	ACBS_TORMA
22	1648	53.0	586	1	ACBS_TORCA
23	1559.5	50.1	617	2	Q67BC2
24	1557.5	50.1	617	2	Q85TM9
25	1455.5	46.8	767	1	ACBS_CHICK
26	1435	46.1	602	2	Q76999
27	1376	44.2	605	2	Q76998
28	1358	43.7	526	2	Q86YX9
29	1323	42.5	701	2	Q75VX9
30	1319	42.4	702	2	Q6A2E2
31	1317	42.3	702	1	ACBS_CULPI

32	1302	41.9	523	2	Q7RTM0
33	1302	41.9	737	1	ACE1_ANOGA
34	1302	41.9	743	2	Q7PUR2
35	1294	41.6	559	2	Q7PKM1
36	1273	40.9	687	2	Q86CZ4
37	1220	39.2	676	2	Q9BMJ1
38	1217	39.1	676	2	Q65Z60
39	1216	39.1	660	2	Q6KAV3
40	1214	39.0	676	2	Q65Z63
41	1213	39.0	671	2	Q6KAV4
42	1212	39.0	676	2	Q8MV35
43	1209	38.9	675	2	Q6KAV5
44	1209	38.9	676	2	Q65Z62
45	1203	38.7	676	2	Q6ECH8

ALIGNMENTS

RESULT 1

CHLE_HUMAN

ID CHLE_HUMAN STANDARD; PRT; 602 AA.

AC P06276;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)

DE (Choline esterase II) (Butyrylcholine esterase)

DE (pseudocholinesterase)

GN Name=BCHE; Synonyms=CHE1;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90212557; PubMed=2322535;

RA Arpagaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,

RA Lockridge O.;

RT "Structure of the gene for human butyrylcholinesterase. Evidence for a

RT single copy.";

RL Biochemistry 29:124-131(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX TISSUE=Fetal;

RC MEDLINE=87231856; PubMed=3035536;

RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreq H.;

RT "Isolation and characterization of full-length cDNA clones coding for

RT cholinesterase from fetal human tissues.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).

RN [3]

RP SEQUENCE FROM N.A.

RX TISSUE=Brain;

RC MEDLINE=89016155; PubMed=3477799;

RA McTierman C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,

RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.;

RT "Brain cDNA clone for human cholinesterase.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).

RN [4]

RP SEQUENCE FROM N.A.

RX TISSUE=Skin;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 29-602.
RC TISSUE=Plasma;
RX MEDLINE=87109144; PubMed=3542989;
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RA Johnson L.L.;
RT "Complete amino acid sequence of human serum cholinesterase.";
RL J. Biol. Chem. 262:549-557(1987).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=88007487; PubMed=3115973;
RA Lockridge O., Adkins S., la Du B.N.;
RT "Location of disulfide bonds within the sequence of human serum
RT cholinesterase.";
RL J. Biol. Chem. 262:12945-12952(1987).
RN [7]
RP REVIEW.
RX MEDLINE=89149758; PubMed=3067729;
RA Lockridge O.;
RT "Structure of human serum cholinesterase.";
RL Bioessays 9:125-128(1988).
RN [8]
RP VARIANT ATYPICAL GLY-98.
RX MEDLINE=89128896; PubMed=2915989;
RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA van der Spek A.F.L., Lockridge O., la Du B.N.;
RT "Identification of the structural mutation responsible for the
RT dibucaine-resistant (atypical) variant form of human serum
RT cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN [9]
RP VARIANT ILE-358.
RX MEDLINE=96287386; PubMed=8680411;
RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA Moriaki K.;
RT "Mutations of human butyrylcholinesterase gene in a family with
RT hypocholinesterasemia.";
RL Hum. Mutat. 6:349-351(1995).
CC -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -!- SURUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -!- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -!- DISEASE: Mutant alleles of CHE1 are responsible for
CC hypocholinesterasemia resulting in suxamethonium sensitivity.
CC Homozygous persons sustain prolonged apnea after administration of
CC the muscle relaxant suxamethonium in connection with surgical
CC anesthesia.
CC -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M32391; AAA99296.1; -;
DR EMBL; M32389; AAA99296.1; JOINED.
DR EMBL; M32390; AAA99296.1; JOINED.
DR EMBL; M16541; AAA98113.1; -;

DR M16474; AAA52015.1; -;
DR EMBL; BC018141; AAH18141.1; -;
DR PIR; A33769; ACHU.
DR PDB; 1EHO; Model; A=30-560.
DR PDB; 1EHQ; Model; A=30-560.
DR PDB; 1POI; X-ray; A=29-557.
DR PDB; 1POM; X-ray; A=29-557.
DR PDB; 1POQ; X-ray; A=29-557.
DR PDB; 1POQ; X-ray; A=29-557.
DR H-InvDB; HGNC:983; BCHE.
DR H-InvDB; HIX003828; -;
DR MIM; 177400; -;
DR GO; GO:0001540; P:beta-amyloid binding; NAS.
DR GO; GO:0003824; P:catalytic activity; NAS.
DR GO; GO:0004104; F:cholinesterase activity; NAS.
DR GO; GO:0019899; F:enzyme binding; NAS.
DR GO; GO:0050783; P:cocaine metabolism; TAS.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00078; CHOLINESTERASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW 3D-structure; Direct protein sequencing; Disease mutation;
KW Glycoprotein; Hydrolase; Polymorphism; Serine esterase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 602
FT ACT SITE 226 226
FT ACT SITE 353 353
FT ACT SITE 466 466
FT DISULFID 93 120
FT DISULFID 280 291
FT DISULFID 428 547
FT DISULFID 599 599
FT CARBOHYD 45 45
FT CARBOHYD 85 85
FT CARBOHYD 134 134
FT CARBOHYD 269 269
FT CARBOHYD 284 284
FT CARBOHYD 369 369
FT CARBOHYD 483 483
FT CARBOHYD 509 509
FT CARBOHYD 514 514
FT VARIANT 98 98
FT VARIANT 271 271
FT VARIANT 358 358
FT VARIANT 418 418
FT VARIANT 567 567
FT VARIANT 567 567
SQ SEQUENCE 602 AA; 68418 MW; C9836403D9057F27 CRC64;
Query Match 99.5%; Score 3096; DB 1; Length 602;
Best Local Similarity 99.8%; Pred. No. 1.9e-224;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EDDIIITKNGKVRGMNLTVFGGVTAFGLIPYAQPPLGRFRPKKPSLTWSDIWNATK 60
Db 29 EDDIIITKNGKVRGMNLTVFGGVTAFGLIPYAQPPLGRFRPKKPSLTWSDIWNATK 88
Qy 61 YANSCCNIDQSPFGFHGSEMNWNTDLSCLYINWIPAPKPNATVLIWYGGGFQT 120
Db 89 YANSCCNIDQSPFGFHGSEMNWNTDLSCLYINWIPAPKPNATVLIWYGGGFQT 148
Qy 121 GTSSLHYVDGKFLARVERVIVVSNRYVGALGFALPCNPEAPGNMGLFDQOLALQWVK 180
Db 149 GTSSLHYVDGKFLARVERVIVVSNRYVGALGFALPCNPEAPGNMGLFDQOLALQWVK 208

Ds	429	EHRSSKLPWPBWMGVHGYEIEFVGLPLERRVNTYKAEIILSRSMKRWANFAKYGNPN	488
Qy	482	ETQNNSTWVPFKSTEQKYLTLNTSTRTMTKLAQQCRFWTSFPFKVLEMTGNIDEAEW	541
Ds	489	GTQNNSTWVPFKSTEQKYLTLNTSTRTMTKLAQQCRFWTLFPFKVLEMTGNIDEABQ	548
Qy	542	EWKAGFHRWNNYMDWKNQFNNDYTSKKESC	573
Ds	549	EWKAGFHRWNNYMDWKNHFNNDYTSKKERCAG	580
RESULT 3			
Q9NIN9	PRELIMINARY; PRT; 602 AA.		
ID	Q9NIN9		
AC	Q9NIN9		
DT	01-OCT-2000	(T-EMBLrel. 15, Created)	
DT	01-OCT-2000	(T-EMBLrel. 15, Last sequence update)	
DT	01-OCT-2003	(T-EMBLrel. 25, Last annotation update)	
DE	Butyrylcholinesterase (EC 3.1.1.8).		
GN	Name=ECHE;		
OS	Equus caballus (Horse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
OX	NCBI_TaxID=9796;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=20181263; PubMed=10718335; DOI=10.1016/S0006-2952(99)00389-5;		
RA	Wierdl M., Morton C.L., Danks M.K., Potter P.M.;		
RT	"Isolation and characterization of a cDNA encoding a horse liver		
RT	butyrylcholinesterase: evidence for CPT-11 drug activation.";		
RL	Biochem. Pharmacol. 59:773-781(2000).		
CC	-1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.		
DR	EMBL; AF178685; AAF61480.1; -.		
DR	HSSP; P06276; IPOP.		
DR	GO; GO:0004104; F:cholinesterase activity; IEA.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	InterPro; IPR002018; CarbesteraseB.		
DR	InterPro; IPR000997; Cholinesterase.		
DR	InterPro; IPR000379; Ser_estrs.		
DR	Pfam; PF00135; Coesterase; 1.		
DR	PRINTS; PR00878; CHOLNESTRASE.		
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.		
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.		
KW	Hydrolase.		
SEQUENCE	602 AA; 68838 MW; 94C73F00431DF26E CRC64;		
Query Match 89.2%; Score 2775; DB 2; Length 602;			
Best Local Similarity 90.7%; Pred. No. 2.9e-200;			
Matches 518; Conservative 19; Mismatches 34; Indels 0; Gaps 0;			
Qy	1	EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAQPPLGRFRFKKQSLTKWSIDWNAIK	60
Ds	29	EEDIIATKNGKVRGMNLTVFGGTVAFLGIPYAQPPLGRFRFKKQSLTKWSIDWNAIK	88
Qy	61	YANSCQNI DOSFGFGHSEMMNNTDLSBCLYLVNWI PAKPKNATVLIWYGGGFQT	120
Ds	89	YANSCYQNTDOSFGFGHSEMMNNTDLSBCLYLVNWI PAKPKNATVLIWYGGGFQT	148
Qy	121	GTSSLHVYDGKFLARVERVIVSMNRYVGALGFLALPGNPEAPNGMGLFDQQLALQWVQK	180
Ds	149	GTSSLVYDYGKFLARVERVIVSMNRYVGALGFLALPGNPEAPNGMGLFDQQLALQWVQK	208
Qy	181	NIAAFGNPKSVTLFGESAGASVSLHLLSPGSHSLFTRAILQSGSNAPWAVTSLYEAR	240
Ds	209	NIAAFGNPKSVTLFGESAGASVSLHLLSPGSHSLFTRAILQSGSNAPWAVTSLYEAR	268
Qy	241	NRTNLAKLTCGSRNENETIICLRNKDQPIILLNEAFVVPYGPVPLSVNFGPTVDGDFLT	300
Ds	269	NRTNLAKLTCGSRNENETIICLRNKDQPIILLNEAFVVPYGPVPLSVNFGPTVDGDFLT	328
Qy	301	DMPDILLBQFKTKTQIILVGNKDEGTWFLVYGPAGFGSKDNNSIITRKEFOEGLKIFPPG	360
Ds	329	DMPDILLBQFKTKTQIILVGNKDEGTWFLVYGPAGFGSKDNNSIITRKEFOEGLKIFPPR	388

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FT CARBOHYD 486 486 N-linked (GlcNAc...).
SQ SEQUENCE 574 AA; 65641 MW; 07755EB9FB9CB33E CRC64;

Query Match
Best Local Similarity 89.2%; Score 2774; DB 1; Length 574;
Matches 517; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGTGTATFLGIPYAQPPLGLRFRFKKPSQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFGTGTATFLGIPYAQPPLGLRFRFKKPSQSLTKWSDIWNATK 60

QY 61 YANSCCONIDQSPFGFHGSEMNPNTDISEDCLYLNVMIPAPKPNATVLIWYGGGQOT 120
DB 61 YANSCYQNTDQSPFGFHGSEMNPNTDISEDCLYLNVMIPAPKPNATVLIWYGGGQOT 120

QY 121 GTSSLHVVDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNMGLFDQQLALQWYQK 180
DB 121 GTSSLVVDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNMGLFDQQLALQWYQK 180

QY 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTLNKLAKTCCSRENETEIIKCLRNKDQPOBILLINEAFVVPYGTPLSVNFGPTVDDGFLT 300
DB 241 NRTLNKLAKTCCSRENETEIIKCLRNKDQPOBILLINEAFVVPYGTPLSVNFGPTVDDGFLT 300

QY 301 DMPDILLELGQFKTKQIILGVNKGDTWFLVVGAPGFSKDNNSIITRKEPQEGKIFPPG 360
DB 301 DMPDITLLQQLQKPKRTQIILGVNKGDTWFLVVGAPGFSKDNNSIITRKEPQEGKIFPPR 360

QY 361 VSEFGKESILFHYTDWDDQRPENTREALGDVVDYNTFCPALETKKFSKSEGNNAFFY 420
DB 361 VSEFGKESILFHYMDWDDQRAENREALDDVVDYNTICPALETKKFSKSELGNDAAFFY 420

QY 421 PEHRSKLPWPBMGVMHGYEIEFVGLPLERRDNYTKAEITLSISIVKRWANFAKYNP 480
DB 421 PEHRSKLPWPBMGVMHGYEIEFVGLPLERRVNYTRABEITLSISIMKRWANFAKYNP 480

QY 481 NETQNNSTWVPFKTEQKYLNTLSTRTIMTKLRAQCCRFWTSFPFKVLEMTGNIDBAE 540
DB 481 NGTQNNSTWVPFKTEQKYLNTLSTESPKYTKLRAQCCRFWTLFPFKVLEMTGNIDBAE 540

QY 541 MEWKAGFHRNNYMDWKNQFNNDYTSKKESC 571
DB 541 REWKAGFHRNNYMDWKNQFNNDYTSKKESC 571
```

RESULT 5

```
CHLE FELCA STANDARD; PRT; 602 AA.
ID CHLE FELCA
AC 062760;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN Name=BCE;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]_TaxID=9685;
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=20334351; PubMed=10874122; DOI=10.1016/S0006-2952(00)00365-8;
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma.";
RL Biochem. Pharmacol. 60:479-487(2000).
```

Query Match 86.7%; Score 2696; DB 1; Length 602;
Best Local Similarity 87.6%; Pred. No. 2.6e-194;
Matches 503; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGTGTATFLGIPYAQPPLGLRFRFKKPSQSLTKWSDIWNATK 60
DB 29 EDDIIATKNGKVRGMNLTVFGTGTATFLGIPYAQPPLGLRFRFKKPSQSLTKWSDIWNATK 88

QY 61 YANSCCONIDQSPFGFHGSEMNPNTDISEDCLYLNVMIPAPKPNATVLIWYGGGQOT 120
DB 89 YANSCYQNTDQSPFGFHGSEMNPNTDISEDCLYLNVMIPAPKPNATVLIWYGGGQOT 148

QY 121 GTSSLHVVDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNMGLFDQQLALQWYQK 180
DB 149 GTSSLVVDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNMGLFDQQLALQWYQK 208

QY 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 209 NIAAFGNGPKSVTLFGESAGAGSVLSHLLSPRQPLFTRAILQSGSFNAPWAVSLDRAK 268

QY 241 NRTLNKLAKTCCSRENETEIIKCLRNKDQPOBILLINEAFVVPYGTPLSVNFGPTVDDGFLT 300
DB 269 NRTLNKLAKTCCSRENETEIIKCLRNKDQPOBILLINEAFVVPYGTPLSVNFGPTVDDGFLT 328

QY 301 DMPDILLELGQFKTKQIILGVNKGDTWFLVVGAPGFSKDNNSIITRKEPQEGKIFPPG 360
DB 301 DMPDITLLQQLQKPKRTQIILGVNKGDTWFLVVGAPGFSKDNNSIITRKEPQEGKIFPPR 360


```
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 597 AA; 67776 MW; 771204D166C7EEAC CRC64;

Query Match
Best Local Similarity 80.5%; Score 2505; DB 2; Length 597;
Matches 458; Conservative 47; Mismatches 69; Indels 0; Gaps 0;

Qy 1 EDDIIATNGKVRGMNLTVPFGTVPFLGIPYAPQPLGLRLRFKKPQSLTKWSDIWNATK 60
Db 24 EEDVIITTKTRVGLSPILGSGVTAPFLGIPYAPQPLGSLRLRFKKPQPLNKPDPVYNATK 83

Qy 61 YANSCQNIDOSFPGFHGSEMNNTDISEDCLYLNWIPAPKPNATVLIWYGGGFOT 120
Db 84 YANSCYQNIQDAFPFGQSEMNNTDISEDCLYLNWIPVPKPNATVMVWYGGGFOT 143

Qy 121 GTSSLHVYDGFKLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQOLALQWVK 180
Db 144 GTSSLPVYDGFKLARVERVIVSMYRVGALGFLAFGNSEAPGNMGLFDQOLALQWVK 203

Qy 181 NIAAFGNPKSVTLFGESAGAASVSLHLLSPGSHLFTTRAILQSGSNAPWAVTSLYEAR 240
Db 204 NIAAFGNPKSVTLFGESAGAASVSLHLLCPQSYPLFTTRAILGSSSNAPWAVKHPBEAR 263

Qy 241 NRTLNKLTCGSRNETETIICKLRNKDPOBILNEAPVVPYGPLSVNFGPTVDGDFLT 300
Db 264 NRTLTAKFICGSKENEBKIIICLRSKDPQBELINEKVLPSDSIRSNFGPTVDGDFLT 323

Qy 301 DMPDILLBLGQFKTKQILVGNKDEGTFWLYVYAGPFGSKONNSIITRKEFOEGLKIFPPG 360
Db 324 DMPHTLLQGLKVAKTQILVGNKDEGTFWLYVYAGPFGSKONNSIITRKEFOEGLNMYFPG 383

Qy 361 VSEFGKSIILPHYTDVDDQRPENYREALGVGDYNPICPALBFTKXFSWGNNAFFYY 420
Db 384 VSSLGKEAILFYVDLQDTPEVYREAFDDIIGDYNIIICPALBFTKXFAELEINAFYY 443

Qy 421 FEHRSSKLPWPEWGMVHGHEIEFVGLPLERRDNYTKAEIILRSIVKRWANFAKYNP 480
Db 444 FEHRSSKLPWPEWGMVHGHEIEFVGLPLERRVNYTRAEIIFRSIMKTWANFAKYGHP 503

Qy 481 NETQNNSTWPFVFKSTEOKYLTLTNTESTRIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 540
Db 504 NGTQNSTWPFVFTSTEOKYLTLTNTEKSKINSKLRAQCQWRLFPFKVLMTGDIIDERE 563

Qy 541 WEWKAGFHRWNNYMDWKNQNFNDYTSKKESCVGL 574
Db 564 QEWKAGFHRWNNYMDWKNQNFNDYTSKKETCTDL 597

RESULT 9
ID Q90ZK8 PRELIMINARY; PRT; 603 AA.
AC Q90ZK8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Butyrylcholinesterase precursor (EC 3.1.1.8).
GN Name=BCHE;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Geisler K., Chatonnet A., Layer P.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AJ306928; CAC37792.1; -.
DR HS8P; P06276; 1P01.
DR GO; GO:0004104; F:cholinesterase activity; IEA.
```



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FT SIGNAL 1 23 Potential.
FT CHAIN 24 633 Acetylcholinesterase.
FT ACT_SITE 225 352 Acyl-ester intermediate (By similarity).
FT ACT_SITE 352 352 Charge relay system (By similarity).
FT ACT_SITE 494 494 Charge relay system (By similarity).
FT DISULFID 91 118 By similarity.
FT DISULFID 279 290 By similarity.
FT DISULFID 427 579 By similarity.
FT DISULFID 630 630 Interchain (By similarity).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 633 AA; 17814 MW; F92FE7E4AD8B4C3 CRC64;

Query Match 56.8%; Score 1765; DB 1; Length 633;
Best Local Similarity 53.2%; Pred. No. 3.6e-124;
Matches 324; Conservative 103; Mismatches 146; Indels 36; Gaps 6;

Qy 1 EDDIIATKNGKVRGMLTVFGGT-VTAFLGIPYAQPPLGLRLPKPKQSUTKWDINWAT 59
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 DPGLTITRLGQVQGTLPVDRSHVIAFLGIPAEPLGKWRPKPKPPKPMNDVFDAR 85
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 60 KYANSCQNIQDSRPFHSGSEWMPNTDLSDDCLYLVWIPA-PKPKNATVLIWYGGF 118
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 86 DYPACQYQVDTSPFGSGTEWMPNRMMSDDCLYLVWVPAIPRPHNLTVMWYGGF 145
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 119 QTGTSSLLHYDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNGLFDQQLAQWV 178
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 146 YSGSSLDVYDGRYLAHSEKVVVSMYRVSAFGFLALNGSAEAPGVNGLLDQLAQWV 205
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 179 QKNIAAFGNGPKSVTLFGESAGASVSLHLSPGSHSLFTRAILQSGSFNAPWVTSIYE 238
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 QDNTHFFGNGPKQVTFGESAGASVGMHLLSPDSRPKFTRAILQSGVPGNPMRTVSFDE 265
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 239 ARNLTNLAKLTGCSRENETEIIKCLRNDKQOEILLNEAFVVPYGTPLSVNFGPTVDGDF 298
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 266 ARRAIKRLGRVLVCPDGDNDTDLICLSKQPDLDIQBLVLPFSGLFRFSFVPIDGV 325
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 299 LTMDPDIILLEGQFKKTLQILGVNKGDEGTFLVYAGPFSKDNNSIITRKEFQGLKIFF 358
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 326 FPDTPPEMLNSGNFKDTILLGVNQNEGSFLYIYAGPFSKDNESLITREDFLQGVMSV 385
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 359 PGVSEFGKESILFHYTDWDDQRENVRALGDVVDYNFICPALEFTFKFSE----- 411
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 386 PHANEIGLEAVILQYTDWMDENPIKREAMDIDVGDHNVVCPQLQHFAPKMYAQYSLQGG 445
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 412 -----NGN-----NAPFYFYEHRSSKLWPPEWGMVGHVEIEFVGLP 449
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 446 TGTASQGNLGNWNGSGASNSQSVSYLYMFDHRASNLVWPENWGVJHGIEIEFVGLP 505
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 450 LERRDNYTKABEILSRISVTKRWANPAKYGPNETQNNSTSD---WPVPKSTEQKYLTLNT 505
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 506 LEKRLNYTLEBKLSRMWKYWANFARTGNPNINVDGSIIDSRRRWPVFTSTEQKHVGLNT 565
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 506 ESTRIMTKLRAQCRFTWSPPKVLEMTGNTIDEAEWEWKAQFHRWNNWMDWKQPFNDYT 565
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 566 DSLVKHKGKQFCALNRFLRLNLVTNIDDAERQWKAEFHRWSSYMHMKQKQFDHY- 624
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 566 SKKESCVGL 574
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 625 SKQRCITNL 633

RESULT 12
ACES_BUNFA STANDARD; PRT; 606 AA.
ID ACES_BUNFA 092035; Q73748; Q10720;
AC Q10720; Q73748; Q10720;
DT 01-NOV-1997 (Rel. 35; Created)
DT 10-OCT-2003 (Rel. 42; Last sequence update)
DT 25-OCT-2004 (Rel. 45; Last annotation update)
```

```
DE OS Acetylcholinesterase precursor (EC 3.1.1.7) (ACHe).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8613;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM S).
RC TISSUE=Venom gland;
RX MEDLINE=96279007; PubMed=8662867; DOI=10.1074/jbc.271.25.15099;
RA Cousin X., Bon S., Duval N., Massoulie J., Bon C.;
RT "Cloning and expression of acetylcholinesterase from Bungarus
fasciatus venom. A new type of COOH-terminal domain; involvement of a
positively charged residue in the peripheral site.";
RL J. Biol. Chem. 271:15099-15108(1996).
RN [2]
RP SEQUENCE OF 512-606 FROM N.A. (ISOFORMS S AND T). SUBUNIT, AND TISSUE
SPECIFICITY.
RC TISSUE=Liver, and Muscle;
RX MEDLINE=98212017; PubMed=9545320; DOI=10.1074/jbc.273.16.9812;
RA Cousin X., Bon S., Massoulie J., Bon C.;
RT "Identification of a novel type of alternatively spliced exon from the
acetylcholinesterase gene of Bungarus fasciatus. Molecular forms of
acetylcholinesterase in the snake liver and muscle.";
RL J. Biol. Chem. 273:9812-9820(1998).
RN [3]
RP SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.
RC TISSUE=Venom;
RX MEDLINE=96244524; PubMed=8674549; DOI=10.1016/0014-5793(96)00447-4;
RA Cousin X., Creminon C., Grassi J., Meflah K., Cornu G., Salou B.,
RT Bon S., Massoulie J., Bon C.;
RL FEBS Lett. 387:196-200(1996).
CC -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -!- CATALYTIC ACTIVITY: Acetylcholine + H2O = choline + acetate.
CC -!- SUBUNIT: Isoform S is monomeric. Isoform T can form oligomers,
including collagen-tailed forms.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=Q92035-2; Sequence=Displayed;
CC Name=S;
CC IsoId=Q92035-1; Sequence=VSP_008215;
CC -!- TISSUE SPECIFICITY: Liver and muscle contain both isoform T and
isoform S. Venom gland predominantly contains isoform S.
CC -!- PM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
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CC -----
CC EMBL; U54591; AAC59905.1; -.
CC EMBL; AF045238; AAC16420.1; -.
CC EMBL; AF045238; AAC16421.1; -.
CC HSP; P04058; 1H23.
CC InterPro; IPR002018; CarboxylesteraseB.
CC InterPro; IPR000997; Cholinesterase.
CC InterPro; IPR000908; Fish_Ache.
CC InterPro; IPR000379; Ser_estrs.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLNESTRASE.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Hydrolyase; Membrane; Neurotransmitter degradation; Serine esterase;
KW Signal; Synapse.
```

FT SIGNAL 1 28 Potential.
FT CHAIN 29 606 Acetylcholinesterase.
FT ACT SITE 231 358 Acyl-ester intermediate (By similarity).
FT ACT SITE 358 358 Charge relay system (By similarity).
FT ACT SITE 471 471 Charge relay system (By similarity).
FT DISULFID 98 125 By similarity.
FT DISULFID 295 296 By similarity.
FT DISULFID 433 522 By similarity.
FT DISULFID 603 603 Interchain (in isoform T) (By similarity).
FT CARBOHYD 289 379 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 564 564 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 567 606 DNIEAEKQWLEFLHWSYMMHWSQDHYNKQRCSEL
FT -> VDPADRRRRGARA (in isoform S).
FT ->FTID=VSP_008215.
FT MUTAGEN 101 101 M->Y: Increases peripheral site ligand binding.
FT MUTAGEN 316 316 K->D: Increases peripheral site ligand binding.
FT CONFLICT 268 268 T -> S (in Ref. 3).
FT CONFLICT 350 350 V -> L (in Ref. 3).
SQ SEQUENCE 606 AA; 68074 MW; B95998AEAE0E5709 CRC64;

Query Match 55.4%; Score 1722.5; DB 1; Length 606;
Best Local Similarity 52.9%; Pred. No. 5.5e-121;
Matches 301; Conservative 110; Mismatches 157; Indels 1; Gaps 1;

QY 3 DIIATKNGKVRGMNLTVPFGTGTAFGLGIPYAPQPLGLRFRKPKQSLTKWSDIMNATKYA 62
DB 36 ELUVSTQTSVGLSLVDLGHVSAPLGLIPFAEPPLGRMRFLRPPVPMQHVLDATYK 95

QY 63 NSCCNQIDQSPFGHSGEMNPNTDLSDELINLVNWIAPKPKNATVLIWYGGGFGTGT 122
DB 96 PACYQWDTSYFGQTEWNNRGNSEDCLYLNIVSPSPKDPVLVWYGGGFGYSGA 155

QY 123 SSLHYVDGKFLARVERVIVSMNRYVGLAFGLALPGNPEAPGNMGLFDQQLALQWQXNI 182
DB 156 ASLDVYDGRFLTYQNVILVSLSYRGAFGLGLPGSPAPGNMGLLDQRLALQWQXNI 215

QY 183 AAFGNPKSVTLFGESAGAAVSLLHLSPGSHSLFTRAILQSGSFNAPWAVTSLYE 242
DB 216 HPFGNPRAVTVFGESAGAAVSVMHLLSTQSRFLQRAILOSGGNAPWATVPAESRGR 275

QY 243 TLNLAKLTGCSRENETEIIKCLRNKDPQBIILLNEAFVVPYGTPLSVNFGPTVDGDFLDM 302
DB 276 AALLGKQLGCHENNSELVSLRKNPQELIDEENSULPYKSI PRFPFVPIVDGDFPDT 335

QY 303 PDILLELGQFKTKQILVGNKDEGTWFLVYGAPGSKNNSTIITRKEFOEGLKIFPPGVS 362
DB 336 PEAMLSNGNFKETQVLLGVVDEGSYFLIYGLPGFSKONESLISRADFLEGVRMSVPHAN 395

QY 363 EFGKESILPHYTDWDDQBPENYREALGDVGDVNYFICPALEFTKFKSEWGNNAFYYPE 422
DB 396 DIATDAVQLQYTDWDDQDNREKREALDDIVGDHNVICPVQFANDYAKRNSKVAYLFD 455

QY 423 HRSSKLPPEWNGVMHGYEIEFVGLPLERRDNYTKABEILSRISVKKWANPAKYGPNNE 482
DB 456 HRASNLNPPWNGVPHGYEIEFVGLPLNDLSNLYTPQEKELSRMRMYANFARTGNPTD 515

QY 483 TQNNSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRWTSFFPKVLEMTGNIDEAEWE 542
DB 516 PADKSGAWPTYTASQVYQLNTQPLATQPSLRQAICAFWNHFLPKLLNATNDIEEAEQ 575

QY 543 WKAGHRWNNYMDKQNFNDYTSKKESC 571
DB 576 WKLEFLHWSAYMMHWSQDHY-NKQDRC 603

RESULT 13

Q67BC1

ID Q67BC1 PRELIMINARY; PRT; 614 AA.

AC Q67BC1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Acetylcholinesterase T-form.
DE Acetylcholinesterase T-form.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Cohen O., Kronman C., Velan B., Shafferman A.;
RA "Macaca mulatta acetylcholinesterase gene";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AY372522; AAR24295.1; JOINED.
DR EMBL; AY372523; AAR24295.1; JOINED.
DR EMBL; AY372526; AAR24295.1; JOINED.
DR EMBL; AY372524; AAR24295.1; JOINED.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00135; Coesterase 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
SQ SEQUENCE 614 AA; 67772 MW; 7A4FCEE096015C5C CRC64;

Query Match 54.4%; Score 1691; DB 2; Length 614;
Best Local Similarity 53.0%; Pred. No. 1.3e-118;
Matches 308; Conservative 102; Mismatches 163; Indels 8; Gaps 5;

QY 1 ED-DIIATKNGKVRGMNLTVPFGTGTAFGLGIPYAPQPLGLRFRKPKQSLTKWSDIMNAT 59
DB 35 EDALLTVTRGRLRGIRLTKTPGGPVSAFLGIPPAEPTGPRRFLPPKPKPMSGVVDAT 94

QY 60 KYANSCCNIDQSPFGHSGEMNPNTDLSDELINLVNWIAPKPKNAT-VLIWYGGGF 118
DB 95 TFSQVCYQVDTLPYGPGEETMNPNRNRELSDELINLVNWIAPKPKNAT-VLIWYGGGF 154

QY 119 QTGTSLLHYVDGKFLARVERVIVSMNRYVGLAFGLALPGNPEAPGNMGLFDQQLALQWV 178
DB 155 YSGASSLDVYDGRFLVQAEARTVLVSMNRYVGLAFGLALPGNPEAPGNMGLFDQQLALQWV 214

QY 179 QKNIAAFGNPKSVTLFGESAGAAVSLLHLSPGSHSLFTRAILQSGSFNAPWAVTSLYE 238
DB 215 QENVAAFGGDTSVTLFGESAGAAVSVMHLLSPSPRGLFHRVLSQSGAPNGPWAIVMGGE 274

QY 239 ARNRTNLAKLTGCG---SRENETEIIKCLRNKDPQBIILLNEAFVVPYGTPLSVNFGPTV 294
DB 275 ARRRATQLAHLVGCPPGGTGGNDTELVAQLTRPAQVLVNNHVLVPGESVFRFSFVPV 334

QY 295 DGDPLTMDPDLLELQFKTKQILVGNKDEGTWFLVYGAPGSKNNSTIITRKEFOEGL 354
DB 335 DGDPLTMDPDLLELQFKTKQILVGNKDEGTWFLVYGAPGSKNNSTIITRKEFOEGL 394

QY 355 KIFPPGVSEFGKESILPHYTDWDDQBPENYREALGDVGDVNYFICPALEFTKFKSEWGN 414
DB 395 RVGVQVSDLAEEAVLHYTDLHPEDPARREALSDVVDHNVVCPVAQLAGRLAAQGA 454

QY 415 NAFYFVFEHRSKLPWPPEWNGVMHGYEIEFVGLPLERRDNYTKABEILSRISVKKWANP 474
DB 455 RVYAYVFEHRASTLSWPLMGMVPHGYEIEFVGLPLERRDNYTKABEILSRISVKKWANP 514

QY 475 AKYGNPNETQN-NSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRWTSFFPKVLEMT 533
DB 515 ARTGDPNEPRDPKAPQMPPTTAGAQVYVSLDLRLPLVRGLRAQACAFWNRFLPKLSAT 574

QY 534 GNIDEAEWKEKAGHRWNNYMDKQNFNDYTSKKESC 574
DB 575 DTLDEAEQWKAERHWRSSYVHWKQDFHY-SKQDRCSDL 614

RESULT 14
ACCS_HUMAN STANDARD; PRT; 614 AA.
ID P22303; Q16169; Q9BXP7;
AC 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=ACHE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088577; PubMed=2263619;
RA Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnat A., Neville L.,
RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,
RA Zakut H.,
RT "Molecular cloning and construction of the coding region for human
RT acetylcholinesterase reveals a G + C-rich attenuating structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
RN [2]
RP SEQUENCE OF 521-614 FROM N.A.
RX MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
RA Wilson M.D., Riener C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TPR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5";
RL Nucleic Acids Res. 29:1352-1365(2001).
RN [3]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=94131004; PubMed=8299725; DOI=10.1006/excr.1994.1039;
RA Karpel R., Ben Aziz-Alvora R., Sternfeld M., Ehrlich G., Ginzberg D.,
RA Taroni P., Clementi F., Zakut H., Soreq H.;
RT "Expression of three alternative acetylcholinesterase messenger RNAs
RT in human tumor cell lines of different tissue origins.";
RL Exp. Cell Res. 210:268-277(1994).
RN [4]
RP PARTIAL SEQUENCE.
RC TISSUE=Erythrocyte;
RX MEDLINE=89232136; PubMed=2714437; DOI=10.1016/0014-5793(89)81352-3;
RA Chajlani V., Derr D., Earles B., Schwell E., August T.;
RT "Purification and partial amino acid sequence analysis of human
RT erythrocyte acetylcholinesterase.";
RL FEBS Lett. 247:279-282(1989).
RN [5]
RP MUTAGENESIS OF CYS-611.
RX MEDLINE=92084699; PubMed=1748670;
RA Velan B., Grosfeld H., Kronman C., Leitner M., Gozes Y., Lazar A.,
RA Flashner Y., Marcus D., Cohen S., Shafferman A.;
RT "The effect of elimination of intersubunit disulfide bonds on the
RT activity, assembly, and secretion of recombinant human
RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
RT mutant.";
RL J. Biol. Chem. 266:23977-23984(1991).
RN [6]
RP MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.
RX MEDLINE=92388112; PubMed=1517212;
RA Shafferman A., Kronman C., Flashner Y., Leitner M., Grosfeld H.,
RA Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
RT "Mutagenesis of human acetylcholinesterase. Identification of residues
RT involved in catalytic activity and in polypeptide folding.";
RL J. Biol. Chem. 267:17640-17648(1992).
RN [7]
RP 3D-STRUCTURE MODELING OF 35-574.
RX MEDLINE=98304745; PubMed=9640563;
RA Felder C.E., Botti S.A., Lifson S., Silman I., Sussman J.L.;
RT "External and internal electrostatic potentials of cholinesterase
RT models.";
RL J. Mol. Graph. Model. 15:318-327(1997).

[8]
X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 36-574.
MEDLINE=20508217; PubMed=11053835; DOI=10.1107/S0907444900010659;
Kryger G., Harel M., Giles K., Toker L., Velan B., Lazar A.,
Kronman C., Barak D., Ariel N., Shafferman A., Silman I.,
Sussman J.L.;
"Structures of recombinant native and E202Q mutant human
acetylcholinesterase complexed with the snake-venom toxin fasciculin-
II.";
Acta Crystallogr. D 56:1385-1394(2000).
[9]
VARIANT BLOOD GROUP YT(B) ASN-353.
MEDLINE=93256075; PubMed=8488842;
Bartels C.F., Zelinski T., Lockridge O.;
"Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
encodes for yt blood group polymorphism.";
Am. J. Hum. Genet. 52:928-936(1993).
-!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
-!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
-!- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.
-!- INTERACTS WITH PRIMA1. The interaction with PRIMA1 is required to
anchor it to the basal lamina of cells and organize into tetramers
(by similarity).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=P22303-1; Sequence=Displayed;
Name=2;
IsoId=P22303-2; Sequence=VSP_001457;
POLYMORPHISM: ACHE is responsible for the Yt blood group system.
The molecular basis of the Yt(a)=Yt1/Yt(b)=Yt2 blood group
antigens is a single variation in position 353; His-353
corresponds to Yt(a) and the rare variant with Asn-353 to Yt(b).
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
-!- DATABASE: NAME=Blood group antigen mutation database;
NOTE=Yt blood group system;
WWW="http://www.bioc.aecom.yu.edu/bgmmt/yt.htm".

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or send an email to license@isb-sib.ch).

EMBL; M55040; AAA68151.1; -.
EMBL; AF312032; AAK21003.1; -.
EMBL; S71129; AAC60618.1; -.
PIR; A39256; A39256.
PDB; 1B41; X-ray; A=36-574.
PDB; 1F80; X-ray; A=32-614.
PDB; 2CLJ; Model; Q=32-574.
SWISS-2DPAGE; P22303; HUMAN.
GeneW; HGNC:108; ACHE.
MIM; 100740; -.
MIM; 112100; -.
GO; GO:0005605; C:basal lamina; NAS.
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0042166; F:acetylcholine binding; NAS.
GO; GO:0003990; F:acetylcholinesterase activity; IMP.
GO; GO:0001540; F:beta-amyloid binding; TAS.
GO; GO:0042803; F:protein homodimerization activity; NAS.
GO; GO:0001507; F:acetylcholine breakdown in synaptic cleft; NAS.
GO; GO:0042982; F:amyloid precursor protein metabolism; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0006260; P:DNA replication; TAS.
GO; GO:0007517; P:muscle development; TAS.
GO; GO:0050714; P:positive regulation of protein secretion; TAS.
GO; GO:0009611; P:response to wounding; TAS.
GO; GO:0007416; P:synaptogenesis; TAS.

DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW 3D-structure; Alternative splicing; Blood group antigen;
KW Direct protein sequencing; Glycoprotein; Hydrolase; Membrane;
KW Neurotransmitter degradation; Polymorphism; Sestine esterase; Signal;
KW Synapse.
FT SIGNAL 1 31 Potential.
FT CHAIN 32 614 Acetylcholinesterase.
FT ACT_SITE 234 234 Acyl-ester intermediate.
FT ACT_SITE 365 365 Charge relay system.
FT ACT_SITE 478 478 Charge relay system.
FT DISULFID 100 127
FT DISULFID 298 303
FT DISULFID 440 560
FT DISULFID 611 611
FT CARBOHYD 296 296
FT CARBOHYD 381 381
FT CARBOHYD 495 495
FT VARSPIC 575 614
Interchain.
N-linked (GlcNAc...) (Potential).
N-linked (GlcNAc...) (Potential).
N-linked (GlcNAc...) (Potential).
DILDAERQWKAEPHRSYVMYHKNQFDHYSKQDRCSDL
-> GMCGAGSAGRGVARGQCNPSSLPLASAPSTCPGFT
HGEAARPLGLPLPLLLHQLLLFLSHLRL (in
isoform 2).
/FTID=VSP_001457.
V -> E (in dbSNP:8286).
/FTID=VAR_011934.
H -> N (in Yt(b) antigen; dbSNP:1799805).
/FTID=VAR_002359.
D->N: Misfolding, absence of secretion.
S->A: Loss of activity.
E->A: Loss of activity.
D->N: Misfolding, absence of secretion.
H->A: Loss of activity.
C->A: Impairment of interchain disulfide
bridge formation.
TURN 38 39
TURN 40 42
TURN 47 49
TURN 51 53
TURN 56 57
TURN 60 67
TURN 69 70
TURN 74 76
TURN 77 78
TURN 82 83
TURN 90 92
TURN 94 94
TURN 99 100
TURN 109 110
TURN 112 115
TURN 116 117
TURN 123 124
TURN 129 135
Query Match 54.3%; Score 1689; DB 1; Length 614;
Best Local Similarity 52.8%; Pred. No. 1.9e-118;
Matches 307; Conservative 104; Mismatches 162; Indels 8; Gaps 5;
QY 1 ED-DIIIIATKNGKVGNNLTVEGTTVTAFLGIPYAPQPLGLRFLRKKPQSLTKWSDINAT 59
DB 35 EDAILTVTRGRLGIRLKTGGPVSAFLGIPFAEPGPRFLPPEPKQPSGV DAT 94
QY 60 KYANSCQNDIOSFPFGHSEMMNPNTDISEDCLYLNWIPAPKPKNAT-VLIWYGGGF 118
DB 95 TFQSVCYQVDTLYPGFEGTEMMNRELSDCLYLNWTPYRPTSPFVLWYGGGF 154
QY 119 QTGTSLLHYDCKFLARVERVIVSMYRVGALGFLALPGNPEARCNMGLFDQALQWV 178
DB 155 YSGASSLDVYDGRFLVQABRTVLVSMYRVGAFGLFALPGSREAFNGVLLDQRLQWV 214

QY 179 QKNIAAFGNGPKSVTLFGESAGAAASVSHLLSPQSHSLFTTRAILQSGSFNAPWATSLYE 238
DB 215 QENVAAGCGDPTSVTLFGESAGAAASVGMHLLSPSPRGIFHRAVLQSGAPNGPWTGNGE 274
QY 239 ARNETLNLAKLTGC-----SRENETEIKLCKRNDKPOEITLLNEAFVVPVGTPLSVNFGPTV 294
DB 275 ARRATQAHLVGCGPPGGTGGNDTVELVACLTRPAQVLVNHEHVLPOESVFRFSFVPV 334
QY 295 DGDFLTMDPDLILGQFKTKQILVGVNKNDEGTWFLVYGAFGFKSKNNNSIITRKEFBQGL 354
DB 335 DGDFLSDTPEALINAGDPHGLQVLGVVKGDSGYFLVYGAFGFKSKNLSISRAEFLAGV 394
QY 355 KIFPGVSEFGKESILFHYTDWDDQRPENYREALGDVGVNFCPALEFTTKFSEWGN 414
DB 395 RVGVQVSDLAEEAVLVHTDLPEDPARLREALSDVGVGHNVVCPVAQAGRLAAQGA 454
QY 415 NAFFVYFEHRSKLPWPEWGMVMEGYETEFVFGPLERRDNYTKAEETLSRSIVKRWANF 474
DB 455 RYAYVFEHRASTLSWPLMGVPHGYETEFIFGLDPSRNYTAEKIFAGRLMYWANF 514
QY 475 AKYGNPNETQN-NSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRFWTSPFPKVLBMT 533
DB 515 ARTGDPNEPRPKAPQWPPYTAGAQYVSLDLRPLEVRGLRAQACAFNNRFLPKLSAT 574
QY 534 GNIDEAEWEWKAGFHRNNYMMQNDQNYTSKSKSCVGL 574
DB 575 DTLDEAERQWKAEPHRSYVMYHKNQFDHY-SKQDRCSDL 614
RESULT 15
ACES RAT
ID ACES RAT STANDARD; PRT; 614 AA.
AC P37136;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=Ache;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM T).
RX MEDLINE=93107932; PubMed=8417155;
RA Legay C., Bon S., Vernier P., Coussen F., Massoulie J.;
RT "Cloning and expression of a rat acetylcholinesterase subunit;
RT generation of multiple molecular forms and complementarity with a
RT Torpedo collagenic subunit.";
RL J. Neurochem. 60:337-346(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS H AND R).
RX MEDLINE=93114454; PubMed=8417973; DOI=10.1016/0014-5793(93)81155-S;
RA Legay C., Bon S., Massoulie J.;
RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
RT acetylcholinesterase.";
RL FEBS Lett. 315:163-166(1993).
CC -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -!- SUBUNIT: Homotrimer; composed of disulfide-linked homodimers.
CC Catalytic forms H (GPI-anchor dimer) and T (asymmetric collagen-
CC tailed), which differ in their C-terminus, account for all types
CC of known AChE forms. Interacts with PRIMA1. The interaction with
CC PRIMA1 is required to anchor it to the basal lamina of cells and
CC organize into tetramers (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=T;
CC IsoId=P37136-1; Sequence=Displayed;
CC Name=H;
CC IsoId=P37136-2; Sequence=VSP_001458;
CC Name=R;

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: July 8, 2005, 11:11:07 ; Search time 19 Seconds
(without alignments)
2906.759 Million cell updates/sec

Title: US-09-748-739A-2_COPY_29_602

Perfect score: 3110

Sequence: 1 EDDIIITKNGKVRGNLTV.....MDWKQNFNDYTSKESCVGL 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3096	99.5	602	1 ACHU	cholinesterase (EC
2	2843	91.4	581	2 C39768	cholinesterase (EC
3	2521	81.1	603	2 S70849	cholinesterase (EC
4	1785.5	57.4	596	1 ACVE	acetylcholinesterase
5	1784.5	57.4	599	1 A38868	acetylcholinesterase
6	1689	54.3	614	2 A39256	acetylcholinesterase
7	1678.5	54.0	614	2 JH0811	acetylcholinesterase
8	1675.5	53.9	614	2 JH0314	acetylcholinesterase
9	1639	52.7	584	2 S48724	acetylcholinesterase
10	1636.5	52.6	583	2 S10712	acetylcholinesterase
11	1455.5	46.8	767	2 S47639	acetylcholinesterase
12	1142	36.7	620	2 A34413	acetylcholinesterase
13	1070.5	34.4	637	2 S66236	acetylcholinesterase
14	1044	33.6	746	2 A25363	acetylcholinesterase
15	1040.5	33.5	691	2 JG0150	acetylcholinesterase
16	1030.5	33.1	664	2 J77990	acetylcholinesterase
17	1012.5	32.6	602	2 T37254	acetylcholinesterase
18	948	30.5	629	2 T37255	acetylcholinesterase
19	937	30.1	584	2 T27009	hypothetical prote
20	930	29.9	607	2 T42399	hypothetical prote
21	893	28.7	532	2 T33842	hypothetical prote
22	754	24.2	532	2 A34329	60K esterase (EC 3
23	753	24.2	141	2 C39768	cholinesterase (EC
24	732	23.5	599	2 A57701	sterol esterase (E
25	729	23.4	597	2 A33668	sterol esterase (E
26	728.5	23.4	559	1 JCS408	carboxylesterase (
27	726	23.3	612	2 A34967	sterol esterase (E
28	724	23.3	141	2 D39768	cholinesterase (EC
29	721	23.2	141	2 C39768	cholinesterase (EC

30	721	23.2	141	2 B39768	cholinesterase (EC
31	718.5	23.1	561	2 S47655	carboxylesterase (
32	715	23.0	554	2 A39060	carboxylesterase (
33	711	22.9	745	2 S13586	triacylglycerol li
34	708.5	22.8	565	2 S10367	carboxylesterase (
35	707	22.7	141	2 C39768	cholinesterase (EC
36	701.5	22.6	557	2 A47162	thiolesterase B (E
37	697.5	22.4	567	1 A41010	cholinesterase (E
38	696.5	22.4	562	2 A55281	carboxylesterase (
39	694.5	22.3	561	2 JC2447	carboxylesterase (
40	690.5	22.2	566	2 S19307	carboxylesterase (
41	690	22.2	549	2 JX0054	carboxylesterase (
42	689	22.2	540	2 A31584	carboxylesterase (
43	680.5	21.9	561	2 S62788	carboxylesterase (
44	675.5	21.7	561	2 S71597	carboxylesterase (
45	666	21.4	956	2 A56920	gliotactin precurs

ALIGNMENTS

RESULT 1

ACHU

N:cholinesterase (EC 3.1.1.8) precursor [validated] - human

N:Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C:Accession: A33769; A33887; A34668; A00772

R:Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.

Biochemistry 29, 124-131, 1990

A:Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single cc

A:Reference number: A33769; MUID:90212557; PMID:2322535

A:Accession: A33769

A:Molecule type: DNA

A:Residues: 'MSVQNLQAGAAACISPKYMIPTCKLHLCRESIN', 1-602 <ARP>

A:Cross-references: UNIPROT:P06276; GB:M32391; GB:J02879

A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra

R:Prody, C.A.; Zevin-Sonkin, D.; Gnatt, A.; Goldberg, O.; Soreq, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987

A:Title: Isolation and characterization of full-length cDNA clones coding for cholineste

A:Reference number: A26613; MUID:87231856; PMID:3035536

A:Accession: A26613

A:Molecule type: mRNA

A:Residues: 1-133, 'D', 135-602 <PRO>

R:McTiernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose

Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987

A:Title: Brain cDNA clone for human cholinesterase.

A:Reference number: A33887; MUID:88016155; PMID:3477799

A:Accession: A33887

A:Molecule type: mRNA

A:Residues: 'MSVQNLQAGAAACISPKYMIPTCKLHLCRESIN', 1-602 <MCT>

A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra

R:Nogueira, C.P.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,

Am. J. Hum. Genet. 46, 934-942, 1990

A:Title: Identification of a frameshift mutation responsible for the silent phenotype of

A:Reference number: A34668; MUID:90252779; PMID:2339692

A:Accession: A34668

A:Molecule type: DNA

A:Residues: 143-145, 'VSNWNIIFTCL' <NOG>

A:Note: frameshift mutant in codon for residue 145 (Gly)

R:Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.

J. Biol. Chem. 262, 549-557, 1987

A:Title: Complete amino acid sequence of human serum cholinesterase.

A:Reference number: A00772; MUID:87109144; PMID:3542989

A:Accession: A00772

A:Molecule type: protein

A:Residues: 29-602 <LOC>

A:Experimental source: plasma

C:Comment: Cholinesterase is present in most cells (except erythrocytes).

C:Genetics:

A:Gene: GDB:BCHE; CHE1

A:Cross-references: GDB:120558; OMIM:177400

A:Map position: 3q26.1-3q26.2

A;Introns: 506/2; 562/1
 C;Function:
 A;Description: hydrolyzes acylcholines to choline and a carboxylic acid
 A;Note: this cholinesterase is highly reactive with organophosphate esters
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
 F;1-28/Domain: signal sequence #status predicted <SIG>
 F;29-602/Product: cholinesterase #status experimental <MAT>
 F;56-556/Domain: cholinesterase homology <CHE>
 F;45;85;134;269;284;369;483;509;514/Binding site: carbohydrate (Asn) (covalent) #status
 F;226/Active site: Ser #status experimental

Query Match 99.5%; Score 3096; DB 1; Length 602;
 Best Local Similarity 99.8%; Pred. No. 2.9e-229;
 Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EDDIIATKNGKVRGMNLTVEGGTDTAFLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60
 Db 29 EDDIIATKNGKVRGMNLTVEGGTDTAFLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 88
 Qy 61 YANSCCQNIQDSFGFHGSEMMNPTDSEDCLYLNWIPAPKPNATVLIWIYGGFQT 120
 Db 89 YANSCCQNIQDSFGFHGSEMMNPTDSEDCLYLNWIPAPKPNATVLIWIYGGFQT 148
 Qy 121 GTSSLHYVDGKFLARVERVIVSMNRYVAGLFGFLALPGNPEAPGNMGLFDQOLALQWVK 180
 Db 149 GTSSLHYVDGKFLARVERVIVSMNRYVAGLFGFLALPGNPEAPGNMGLFDQOLALQWVK 208
 Qy 181 NIAAFGPNPKSVTLFGESAGAASVSLHLLSPGSHLFTTRAILQSGSNAPWAVTSLYEAR 240
 Db 209 NIAAFGPNPKSVTLFGESAGAASVSLHLLSPGSHLFTTRAILQSGSNAPWAVTSLYEAR 268
 Qy 241 NRTNLAKLTCGSENETEIIKCLRNDKDPQIILNEAFVVPYGTPLSVNFGPTVDGDLT 300
 Db 269 NRTNLAKLTCGSENETEIIKCLRNDKDPQIILNEAFVVPYGTPLSVNFGPTVDGDLT 328
 Qy 301 DMPDILLELGQFKTKTQILVGNKDEGTWFLVYAGPGSKNNNSITRKEFOEGLKIFPPG 360
 Db 329 DMPDILLELGQFKTKTQILVGNKDEGTWFLVYAGPGSKNNNSITRKEFOEGLKIFPPG 388
 Qy 361 VSEFGKESILPHYTDWDDQRPENYREALGVGDYNYFICPALEFTKKFSEWGNNAFFYY 420
 Db 389 VSEFGKESILPHYTDWDDQRPENYREALGVGDYNYFICPALEFTKKFSEWGNNAFFYY 448
 Qy 421 FEHRSSKLPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISVKRWANFAKYGNP 480
 Db 449 FEHRSSKLPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISVKRWANFAKYGNP 508
 Qy 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 540
 Db 509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 568
 Qy 541 WEWKAGFHRMNNYMDWKNQFNNDYTSKESCVGL 574
 Db 569 WEWKAGFHRMNNYMDWKNQFNNDYTSKESCVGL 602

RESULT 2
 C39768
 cholinesterase (EC 3.1.1.8) - rabbit
 N;Alternate names: butyrylcholinesterase
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C;Accession: S10255; C39768
 F;Jbilo, O.; Chatonnet, A.
 Nucleic Acids Res. 18, 3990, 1990
 A;Title: Complete sequence of rabbit butyrylcholinesterase.
 A;Reference number: S10255; MUID:90326526; PMID:2374720
 A;Accession: S10255
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-581 <JBI>
 A;Cross-references: UNIPROT:P21927; EMBL:X52090; NID:g1476; PIDN:CAA36308.1; PID:g137024

R;Apagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogi
 J. Biol. Chem. 266, 6966-6974, 1991
 A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase
 A;Reference number: A39768; MUID:91201348; PMID:2016308
 A;Accession: C39768
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 75-215 <ARP>
 A;Cross-references: GB:M62779; NID:g164788; PIDN:AAA31169.1; PID:g164789
 C;Genetics:
 A;Introns: 485/2; 541/1
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; glycoprotein
 F;35-535/Domain: cholinesterase homology <CHE>

Query Match 91.4%; Score 2843; DB 2; Length 581;
 Best Local Similarity 92.0%; Pred. No. 6.8e-210;
 Matches 526; Conservative 12; Mismatches 34; Indels 0; Gaps 0;
 Qy 2 DDIIITATKNGKVRGMNLTVEGGTDTAFLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATKY 61
 Db 9 EDVIIITKNGRIGINLPVEGGTDTAFLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATKY 68
 Qy 62 ANSCCQNIQDSFGFHGSEMMNPTDSEDCLYLNWIPAPKPNATVLIWIYGGFQT 121
 Db 69 ANSCCQNIQDSFGFHGSEMMNPTDSEDCLYLNWIPAPKPNATVLIWIYGGFQT 128
 Qy 122 TSSLHYVDGKFLARVERVIVSMNRYVAGLFGFLALPGNPEAPGNMGLFDQOLALQWVK 181
 Db 129 TSSLHYVDGKFLARVERVIVSMNRYVAGLFGFLALPGNPEAPGNMGLFDQOLALQWVK 188
 Qy 182 IAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHLFTTRAILQSGSNAPWAVTSLYEAR 241
 Db 189 IAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHLFTTRAILQSGSNAPWAVTSLYEAR 248
 Qy 242 RTNLAKLTCGSENETEIIKCLRNDKDPQIILNEAFVVPYGTPLSVNFGPTVDGDLT 301
 Db 249 RTNLAKLTCGSENETEIIKCLRNDKDPQIILNEAFVVPYGTPLSVNFGPTVDGDLT 308
 Qy 302 DMPDILLELGQFKTKTQILVGNKDEGTWFLVYAGPGSKNNNSITRKEFOEGLKIFPPG 361
 Db 309 DMPDILLELGQFKTKTQILVGNKDEGTWFLVYAGPGSKNNNSITRKEFOEGLKIFPPG 368
 Qy 362 VSEFGKESILPHYTDWDDQRPENYREALGVGDYNYFICPALEFTKKFSEWGNNAFFYY 421
 Db 369 VSEFGKESILPHYTDWDDQRPENYREALGVGDYNYFICPALEFTKKFSEWGNNAFFYY 428
 Qy 422 EHRSSKLPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISVKRWANFAKYGNP 481
 Db 429 EHRSSKLPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISVKRWANFAKYGNP 488
 Qy 482 ETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 541
 Db 489 ETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 548
 Qy 542 WEWKAGFHRMNNYMDWKNQFNNDYTSKESCVG 573
 Db 549 WEWKAGFHRMNNYMDWKNQFNNDYTSKESCVG 580

RESULT 3
 S70849
 cholinesterase (EC 3.1.1.8) - mouse
 N;Alternate names: butyrylcholine esterase
 C;Species: Mus musculus (house mouse)
 C;Date: 28-Oct-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
 C;Accession: S70849; S15680; A39768
 R;Taylor, P.
 submitted to the EMBL Data Library, August 1992
 A;Reference number: S70849
 A;Accession: S70849
 A;Molecule type: nucleic acid
 A;Residues: 1-603 <TAY>

RESULT 4
ACRYE
N;Alternate names: acetylcholinesterase, EC 3.1.1.7 precursor, IIS form [validated] - Pacific electric ray
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 17-Mar-1987 #sequence revision 08-Nov-1996 #text change 09-Jul-2004

C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a cholinesterase occurs on the outer surfaces of cell membranes, including those of erythrocytes. The 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of C;Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of C;Function: A;Description: hydrolyzes acetylcholine to choline and acetate
A;Pathway: neurotransmitter degradation
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>
F;51-551/Domain: cholinesterase homology <CHE>
F;80,478,554/Binding site: carboxydrate (Asn) (covalent) #status predicted
F;88-115,275-286,423-542/Disulfide bonds: #status experimental
F;105/Binding site: substrate (Trp) #status experimental
F;221/Active site: Ser #status experimental
F;348,461/Active site: Glu, His #status predicted
F;437/Binding site: carboxydrate (Asn) (covalent) #status experimental
F;593/Disulfide bonds: interchain #status experimental

Query Match	57.4%	Score 1785.5	DB 1	Length 596
Best Local Similarity	54.0%	Pred. No. 8.4e-123		
Matches	309	Conservative 109	Mismatches 153	Indels 1
Qy	3	DIIIATKNGKVRGMNLTVFGCTVTAFLGIPYAQPLGRLRFPKQSLTKWSDINWATKYA	62	
Db	26	ELLVNTXSGKVGTRVPLVSLSHISAFUGIPPAEPVGVNRRPRRPBPKPWGVMMNASTYP	85	
Qy	63	NSSCQNIDQSPFGPHSGSEMMNPNTDLSBDCLYLNWVIPAPKPKNATVLIIWYGGGFGTGT	122	
Db	86	NNCQOYVDEQPGFGSGSEMMNPREMSEDCLYLIWVPSRPKSTTVMWIYGGGFYSGS	145	
Qy	123	SSLHYDGKFLARVERVIVGWNTRYVGAFLALPGNDEAPCNMGLFPOQALALQWQXNI	182	
Db	146	STLDVYNGKYLAYTEEVVLVSRYRVAGFGLALHGSQEAFCNVGLLDQRMALQWHDNI	205	
Qy	183	AAFGENPKSVTLFGEAGAAVSUHLHSLPSGSHSLFTRAILQSGSFPNAPWATVLSYEARNR	242	
Db	206	QFQGGDPKTVIIFESAGGASVGHMILSPGSRDIFRRAILQSGSPNCWASVSVAEGRRR	265	
Qy	243	TLNLAKUTGCSRENETEIIKCLRNNKDPQEIILLNEAFVVPYGTPIISVNFQPTVDGDFLDM	302	
Db	266	AVELGRNLNCLNSDEELIHLCKREKKPQELIDVEWNVLPFDSIIFRFSVPVVIDGEFFPTS	325	
Qy	303	PDILLEGQFKKTOILLGVNKDEGTFWLYVAGPFGSKDNNSIITRKEFOEGLKIFPFGVS	362	
Db	326	LESMLNSGNFKTQILLGVNKDEGSFFLYVAGPFGSKDSKISKEDPSMGVSGVSPHAN	385	
Qy	363	EFKGESILFHYTDWDDORPENYREALGDVVDYNYFICPALEFTKFKFSEWGNAPFYIFE	422	
Db	386	DLGLDAVTLQYTDWDDNNGIKNRDGLDIDVDHNVICPLMHFVNYKYTKFNGTLYLYFN	445	
Qy	423	HRSKLPMPEWGVWGHGYEIEBFVGLPLERDNDYTKABEIIISRSIIXKWANPAFKYGNPNE	482	
Db	446	HRASNLVMPPEWGVWGHGYEIEBFVGLPLVKEVLNVTABEALSRRIMHYWATFAKTGNENE	505	
Qy	483	TQNNSTSWPVFKSTEOKYLTALNTSTRTWTKLRAQQCRFWTSFPFKVLEMTGNIDEAEWE	542	
Db	506	PHSQESKWPFLTTEKQKFLDINTBPMKVBQRLRVQMCFVWQFLPKLNATETIDEAERQ	565	
Qy	543	WKAGFHRNNNTYMDWKNQFNNDYTSKKSCVGL	574	
Db	566	WKTFFHRWSSVMMHWKKNQFDHY-SRHRSCAEI	596	

RESULT 5

A38868

acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray

C/Species: Torpedo marmorata (marbled electric ray)

C/Date: 23-Apr-1993 #sequence revision 15-Nov-1996 #text_change 09-Jul-2004

C/Accession: A38868; A29682; S15696; A25650

R/Massoulié, J.; Bon, S.

submitted to the EMBL Data Library, June 1992

A/Reference number: A38868

A:	Accession: A3868
A:	Molecule type: mRNA
A:	Residues: 1-59 <MAS>
A:	Cross-references: UNIPROT:P07692; EMBL:X05497; NID:g64414; PIDN:CAA29047.1; PID:g64415
R:	Sikorav, J.L.; Krejci, E.; Massoulie, J. EMBO J. 6, 1865-1873, 1987
A:	Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of t
A:	Reference number: A29682; MUID:8004392; PMID:2820709
A:	Accession: A29682
A:	Molecule type: mRNA
A:	Residues: 1-40,'G','42'-226,'G','228'-272,'G','274'-284,'E','286'-420,'N',422-599 <SIK>
A:	Cross-references: EMBL:X05497
R:	Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krcijci, B.; Legay, C.; Osterlund, M.; EMBO J. 7, 2983-2993, 1988
A:	Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo elec
A:	Reference number: S01293; MUID:89030590; PMID:3181125
A:	Accession: SI5696
A:	Molecule type: mRNA
A:	Residues: 526-599 <SII>
A:	Cross-references: EMBL>X13172; NID:g64416; PIDN:CRAA31570.1; PID:g64417
A:	Experimental source: clone pACHE2
R:	Bon, S.; Chang, J.Y.; Strosberg, A.D. FEBS Lett. 209, 206-212, 1986
A:	Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-solu
A:	Inesterase.
A:	Reference number: A91370; MUID:87080761; PMID:3792544
A:	Accession: A25650
A:	Molecule type: protein
A:	Residues: 25-40,'G','42'-47 <BON>
C:	Genetics:
A:	Gene: ACHE
C:	Function:
A:	Description: hydrolyzes acetylcholine to choline and acetate
A:	Pathway: neurotransmitter degradation
C:	Superfamily: cholinestrase; cholinestrase homology
C:	Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmi
F:	1-24/Domain: signal sequence #status predicted <SIG>
F:	25-599/Product: acetylcholinestrase #status predicted <MAT>
F:	554-Domain: cholinestrase homology <CHE>
F:	83,440,481,557/Binding site: carbohydrate (asn) (covalent) #status predicted
F:	91-118,278-289,426-545/Disulfide bonds: #status predicted
F:	224,331,464/Active site: Ser, Glu, His #status predicted
F:	596/Disulfide bonds: interchain #status predicted
Qy	Query Match 57.4%; Score 1784.5; DB 1; Length 599; Best Local Similarity 53.8%; Pred No. le=128; Matches 309; Conservative ill; Mismatches 153; Indels 1; Gaps 1;
Db	1 EDDIITATNGKVGRMNLTVFGTGTAFILGPYAQPPLGLRFLFKPKQSITKMSDINWTK 60 : :::: :: :: ::::: :: :: :: :: :: :: :: :: :: : 27 DSELLVNTSKGVMTRIPLSSHISAFILGFPAEPVPVGMMFRDEPPKKPWSGVNNAST 86
Qy	61 YANSCQNIDSGFPFHGSSEMNPNPTDISEDCLYLNWIAPKPKNATVLNIWTGGFQT 120 : :::: :: :: ::::: :: :: :: :: :: :: :: : 87 YPNNCQQVDGEQFFPGPSSEMNPNREMSDCLYLINIWSPRPKSATVMLTYYGGFYVS 146
Qy	121 GTSSIHHVYDGKFARVERVIIVSMNVRYCALGFALPGNPPEAGNMGLFDQQLAQWVK 180 : :::: :: :: ::::: :: :: :: :: :: :: :: : 147 GSSTLDVVNGKYLATVEEVLSLRGAFTLGHSQEAPGNMGLLDQRNALOWVHD 206
Qy	181 NIAAFGGNKPVTLTFGESAGAASVSLHLSPGSHSLFTRAILQGSGFNAPVAVTSLYEAR 240 : :::: :: :: ::::: :: :: :: :: :: :: :: : 207 NIQFFGDPIKTTLTFGESAGRASVGMHIILPCSRDLFREAIILQSGSPNCWPASVSAEGR 266
Qy	241 NRTUNLAKLTCGRESNETETIKLRNKDPQELLNEAFVVPYTPLSVNFPGTPVDGFLT 300 : :::: :: :: ::::: :: :: :: :: :: :: :: : 267 RRAVELRLNLCNLSDEDLIQCIREXKPOELIDVENWNLPDFDISIFRFSPVPVIDGEFFP 326
Qy	301 DMPIILLELGOKFTOILLGVYNKDGTFLVYGAGCFSGDKDNNSILTKEFOEQCLKIFFPQ 360 : :::: :: :: ::::: :: :: :: :: :: :: :: : 327 TSLSELMAAGNFKTKTIILLGVNKGDSGFSLLYLGYGPFCKDSKESIRDFMSGVKLVSPH 386
Qy	361 VSEFGKESIHFHYTDWDQDRPYENTREALGDVVGVGYNFICPALEFTKFSSEGNNAFFY 420

336 GDFLSDTPDALINTGDFQDLQVLGVVVKDEGSFLVYGVPGFSGKDNESLISRAQFLAGVR 395
356 IFFPGVSEFGKESILFHYTDMVDQDORPENYREALGDVVGDVNFICPALEFTKKFSEWGN 415
396 IGVPQASDLAAEA VVLHYTDMWHPEDFAHURDAMS AVVGDHNVVCPVAQLAGRLAAQGAR 455
416 AFFYFHRSSKLPWPBMGMVHGHEIEFFVGLPLERRDNYTKAEELSRISVKRWANFA 475
456 VYAI FHRASLTWPLWGMVPHGYEIEFFVGLPLDSLNVTYERIFAQRLMKYWTNFA 515
476 KYGNPNETQNN-STSWPVFKSTEOKYLTNTLNTSTRIMTKLRAQOCRFWTFFPKVLEMTG 534
516 RTGDPNDPRDSKSPWPPTTAAQYVSLNKLPLEVRRLGRLAQTCAFWNRFLPKLLSATD 575
535 NIDEAEWKA GFHRNNYMDKNOFNDYTSKKESCVGL 574
576 TLDEAEQWKA EFHRSSVMVHWKQPDHY-SKQERCSDL 614

RESULT 8
JH0314
acetylcholinesterase (EC 3.1.1.7) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JH0314
R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternative transcripts
A:Reference number: JH0314; MUID:90380429; PMID:2400605
A:Accession: JH0314
A:Molecule type: mRNA
A:Residues: 1-614 <RAC>
A:Cross-references: UNIPROT:P21836; EMBL:X56518; NID:G49844; PID:CAAG39867.1; PID:G49845
A:Experimental source: brain
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-614/Product: acetylcholinesterase #status predicted <MAT>
F:63-569/Domain: cholinesterase homology <CHE>
F:100-127,288-303,440-560/Disulfide bonds: #status predicted
F:234/Active site: Ser #status predicted
F:296,381,495/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 53.9%; Score 1675.5; DB 2; Length 614;
Best Local Similarity 52.8%; Pred. No. 2.4e-120;
Matches 306; Conservative 104; Mismatches 163; Indels 7; Gaps 4;

Qy 1 EDDIIITKNGKVRGMNLTVEGGTVTAFLGIPYAQPPLGLRLRFPKQPSLTKWSDIMNATK 60
Db DPQLLVVRGQLRGIRLKA PGVPVSAFLGIPFAEPVPGSRFRFPPEPKRPWSGVLDATT 95
Qy 61 YANSCCQNIQDSFGFHGSEMNNTDLSDCLYLNWIPAPKPKNAT-VLIWYGGGFQ 119
Db FQNVICYQVDTLYPGFEGTEMMNPNRELSDCLYLNWTPYPRASPTPVLWYGGGFY 155
Qy 120 TGTSSLHYVDGKFLARVERVIVSMNRYVAGLFGALPGNPAQNMGLFDQQLALQWV 179
Db SGAASLDVYDGRFLAQVEGAVLVSNNYRVGTGFLALPGSREAGNVGLLDQRLALQWV 215
Qy 180 KNIAAFGNGPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILQSGSFNAPWATVSLYE 239
Db ENIAAFGDPMSVTLFGESAGAASVGMHLSLPSRSLFHRVAVLQSGTPNGPWATVSAGEA 275
Qy 240 RNRITLNAKLTCG----SRENETEIIKLRNKDQEIILNEAFVVPYGTPLSVNFGPTVD 295
Db RRRATLLARLVGCPGGAGGNDTELACLRTPAQDLVDHEHWLPOESIFRFSFVPVVD 335
Qy 296 GDFLTMDPDIILELGQFKKTKQILVGVNKDEGTWFLVYAGFSGKDNNSIITRKEFQGLK 355
Db GDFLSDTPALINTGDFQDLQVLGVVVKDEGSFLVYGVPGFSGKDNESLISRAQFLAGVR 395
Qy 356 IFFPGVSEFGKESILFHYTDMVDQDORPENYREALGDVVGDVNFICPALEFTKKFSEWGN 415

396 IGVPQASDLAAEA VVLHYTDMWHPEDFTHLRDAMS AVVGDHNVVCPVAQLAGRLAAQGAR 455
416 AFFYFHRSSKLPWPBMGMVHGHEIEFFVGLPLERRDNYTKAEELSRISVKRWANFA 475
456 VYAI FHRASLTWPLWGMVPHGYEIEFFVGLPLDSLNVTYERIFAQRLMKYWTNFA 515
476 KYGNPNETQNN-STSWPVFKSTEOKYLTNTLNTSTRIMTKLRAQOCRFWTFFPKVLEMTG 534
516 RTGDPNDPRDSKSPWPPTTAAQYVSLNKLPLEVRRLGRLAQTCAFWNRFLPKLLSATD 575
535 NIDEAEWKA GFHRNNYMDKNOFNDYTSKKESCVGL 574
576 TLDEAEQWKA EFHRSSVMVHWKQPDHY-SKQERCSDL 614

RESULT 9
S48724
acetylcholinesterase - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
C:Accession: S48724
R:Jbilo, O.; L'Hermite, Y.; Tulesa, V.; Toutant, J.P.; Chatonnet, A.
Eur. J. Biochem. 225, 115-124, 1994
A:Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue
A:Reference number: S48724; MUID:95010096; PMID:7925428
A:Accession: S48724
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-584 <JBI>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: glycoprotein
F:32-539/Domain: cholinesterase homology <CHE>

Query Match 52.7%; Score 1639; DB 2; Length 584;
Best Local Similarity 51.5%; Pred. No. 1.4e-117;
Matches 299; Conservative 106; Mismatches 168; Indels 8; Gaps 5;

Qy 1 EDDIIITKNGKVRGMNLTVEGGTVTAFLGIPYAQPPLGLRLRFPKQPSLTKWSDIMNATK 60
Db 5 DPQLLVVRGQLRGIRLKA PGVPVSAFLGIPFAEPVPGSRFRFPPEPKRPWAGVLDATA 64
Qy 61 YANSCCQNIQDSFGFHGSEMNNTDLSDCLYLNWIPAPKPKNAT-VLIWYGGGFQ 119
Db FQNVICYQVDTLYPGFEGTEMMNPNRELSDCLYLNWTPYPRPTSPVPLWYGGGFY 124
Qy 120 TGTSSLHYVDGKFLARVERVIVSM-NYRVAGLFGALPGNPAQNMGLFDQQLALQWV 178
Db SGAASLDVYVGRFLVQABGTVLVAMHNYRVGAFGFTCLPGSREAPGNVGLDQRLALQWV 184
Qy 179 QKNIAAFGNGPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILQSGSFNAPWATVSLYE 238
Db QENVAAFGDPASVTLFGESAGAASVGLHLSLPSRGLFHRVAVLQSGAPNGPWATVGVGE 244
Qy 239 ARNRTLNAKLTCG----SRENETEIIKLRNKDQEIILNEAFVVPYGTPLSVNFGPTV 294
Db ARRRATLLARLVVCPGGAGGNDTELVA CLRTPAQDLVDHWRVLPQESIFRFSFVPV 304
Qy 295 DGDFLTMDPDIILELGQFKKTKQILVGVNKDEGTWFLVYAGFSGKDNNSIITRKEFQGL 354
Db GDFLSDTPALINTGDFQDLQVLGVVVKDEGTWFLVYAGFSGKDNESIFRQAFLAGV 364
Qy 355 KIFPPGVSEFGKESILFHYTDMVDQDORPENYREALGDVVGDVNFICPALEFTKKFSEWGN 414
Db RVGVQASDLAAEA VVLHYTDMWHPEDPARLDALSDVGDHNVVCPVAQLAGRLAAQGA 424
Qy 415 NAFYFHRSSKLPWPBMGMVHGHEIEFFVGLPLERRDNYTKAEELSRISVKRWANF 474
Db RVYAYVFEHRASTLSWPLWGMVPHGYEIEFFVGLPLEPSLNTYSEERIFAQRLMYWANF 484
Qy 475 AKYGNPNETQNN-STSWPVFKSTEOKYLTNTLNTSTRIMTKLRAQOCRFWTFFPKVLEMT 533
Db ARTGDPNEPRDAKAPPPPTAGAQYVSLNLRPLEVRRLGRLAQTCAFWNRFLPKLLSAT 544

Qy	534	GNIDEAEWEWKAGFHRWNNYMDWKQFNDYTSKESCVGL	574
		: : : : : : :	
Db	545	DTLDEAERQWKAEFHRWSSYMVHVWKNQFDHY-SKQDRCSDL	584

RESULT 10

S10712

acetylcholinesterase (EC 3.1.1.7) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Nov-1993 #sequence revision 23-Mar-1995 #text_change 12-May-1995
C:Accession: S10712; A39734; B39734; B25650
R:Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, M.K.
FEBS Lett. 266, 123-127, 1990
A:Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and its
A:Reference number: S10712; MUID:90306335; PMID:2365060
A:Accession: S10712
A:Molecule type: protein
A:Residues: 1-583 <DOC>
A:Experimental source: fetal serum
R:Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberg, T.L.
J. Biol. Chem. 265, 7481-7487, 1991
A:Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit dis
A:Reference number: A39734; MUID:91210255; PMID:2019579
A:Accession: A39734
A:Molecule type: protein
A:Residues: 1-15, 'R', 17-38, 225-235, 'X', 237-244, 248-264, 'X', 266-273, 365-380; 396-404, 'X', 4
A:Experimental source: brain, erythrocyte
A:Accession: B39734
A:Molecule type: protein
A:Residues: 1-38 <RO2>
A:Experimental source: fetal serum
R:Bon, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-solu
in:sterase.
A:Reference number: A91370; MUID:87080761; PMID:3792544
A:Accession: B25650
A:Molecule type: protein
A:Residues: 'XS', 3-12 <BON>
A:Experimental source: caudate nucleus
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:32-580/Domain: cholinesterase homology <CHE>
F:61, 265, 350, 464, 541/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:203/Active site: Ser #status predicted

Query Match	52.6%;	Score	1636.5;	DB 2;	Length	583;			
Best Local Similarity	51.7%;	Pred. No.	2.1e-117;						
Matches	300;	Conservative	103;	Mismatches	170;	Indels	7;	Gaps	4
Qy	1	EDDIIITATKNGKVRGMNLTVFGGTYTAFGLGIPYAQPLGLRLRFRKKPQSLTKWSDIWNATK	60	:	:	:	:	:	:
Db	5	DPSELLVMVRGGELURGLRLMAPRGPVSALFLGIPFAEPVPVGRPRFLPBPKPFPWPGVLNATA	64	:	:	:	:	:	:
Qy	61	YANSCQNTIDQSPFGPHGSEMNPNTLSDCLYLNVMIAPKPKNAT-VLIWYGGGFQ	119	:	:	:	:	:	:
Db	65	FQSVCCYQYVDLYPCFEGTEGMNPNRELSDCLYLNVWTPYPRSSFTPLVWYGGGFY	124	:	:	:	:	:	:
Qy	120	TGTSLSHHVYDGKFLARVERIVVSNMYRVGALGPLALPGNDEAPGNMGLFDQOALQWVQ	179	:	:	:	:	:	:
Db	125	SGASSLDVVDGRFLVQAEGTVLVSNNYRVGAFGLALPGSREAPGNVGLLDQRLAQSVQ	184	:	:	:	:	:	:
Qy	180	KNTAAFGGNPKSVTLPGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAPMAVTSIYEA	239	:	:	:	:	:	:
Db	185	ENVAARFGGDOPTSVTLPGESAGAASVGMHLLSPGRGLFHRAVLQSGAPGNPMATVGVGEA	244	:	:	:	:	:	:
Qy	240	NRRTLLNKLITGC- ---SRENETEYIKCLRKNKDQEILLNEAFVVPYGTPLSNFPGPTVD	295	:	:	:	:	:	:
Db	245	RRRATLLARLVCPGCGAGNDTELVACLRRAPQDLVDHEWRVLPQEHVFRFSFVPVVD	304	:	:	:	:	:	:
Qy	296	GDFLTDMPIILLLELQFKKTIQLVGNVKDBGTWFLVYAGPGFSKNNNSIITRKEPQGLK	355	:	:	:	:	:	:
Db	305	GDFLSDTPBALINAGDFVGLQVLVGVWKBEGSYFLVYAGPGFSKDNESLLSRAQFLAGVVR	364	:	:	:	:	:	:

```

356 Qy IFFPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYNYFICPALEFTTKFSEWGN 415
365 Db VGVQPASDLAAEAIVLHYTDLHPEDPARWREALSDVVDGHNVCVAQLAGRLAAQGAR 424
416 Qy AFFYFHEHRSKLPWPMWGMVHGVEIEFVFGLPLEERDNTYKAEIILSRSLVKWANFA 475
425 Db VYAIIFERASTLSWPLWMGVPHGVEIEFIFGLPLEPSLNTYIEBRTFAQLRLMYWANFA 484
476 Qy KYGNPNETQ-NNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFPFKVLEMTG 534
485 Db RTGDNDPNRAPKAPQWPYPYTAGAQYVSLNLRPLGVPQASRAQACAFWNRFPLPKLINATD 544
535 Qy NIDEAEWEWKAGFRHNNYMMDKNQFNNDYTSKKESCVCGL 574
545 Db TLDABERQWKAERHRSYIMVHWKNQFDHY-SKQDRCSDL 583

RESULT 11
S47639
acetylcholinesterase (EC 3.1.1.7) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S47639
R:Randall, W. R.; Rimer, M.; Gough, N. R.
Biochim. Biophys. Acta 1218, 453-456, 1994
A:Title: Cloning and analysis of chicken acetylcholinesterase transcripts from
A:Reference number: S47639; MUID:9432359; PMID:8049273
A:Accession: S47639
A:Molecule type: mRNA
A:Residues: 1-767 <RAN>
A:Cross-references: UNIPROT:P36196; EMBL:U03472; NID:G623031; PIDN:AAA60456.1;
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

```

Query Match	45.8%	Score 1455.5	DB 2	Length 767
Best Local Similarity	39.4%	Pred. No. 2.4e-103		
Matches	291	Conservative 87	Mismatches 188	Indels 173
				Gaps 6
Qy	6	IATKNGKVRGNMLIV--FGGTVTAFGLGIPYAQPPLGRIRFKKPSQL-TKMSDIWNATKYA	62	
Db	32	VRTTGSVRGLLIIPAGPSGSTAAAFGLGIPFAVPLPLGRFRPPLPIPTPTWTCIRDADSQP	91	
Qy	63	NSSCQNTDQSPGPHGSEMMNPNTDLSBDCLYLNWVWPAPKPKNATVLIWIYGGGFQTC	122	
Db	92	FACYQMVDYTTFPFGQSGSEMMNPNEMSBDCLYLNWVTKQDPTTEPVLVIWIYGGGF	151	
Qy	123	SSLHVYDGKFLARVERVIVVSMYRVGALGFALIPGNPEAPGNMGLFDQOLALQWQKNI	182	
Db	152	VSLDVIQRYLAAABEAVVVSMTYRVSGLGFALAGHRDAPGNVGLWQRLALQWRDNA	211	
Qy	183	AAFQGNPKSVTLFCESGAASVSUHLISPGSHSLFTRAILQSGSFNAPWATSLYEARNR	242	
Db	212	EAFQGDPDILTLFCESGAASVGFHLLISPHSKGLFRRAVLQSGSPNGPWATIGAAEGR	271	
Qy	243	TLNLAKUTGCSRENETIILKLRNKDQOEILLNEAFVVPYGTPLSVNPGPTVDGFLTDM	302	
Db	272	AAALGRAVGCYPGNETEFLGCLRGKEAADVLEGGVWMPQSVFRFAFVVPVDDGFVDS	331	
Qy	303	PDILLELQF-----	312	
Db	332	PDVAL-WGDYGVKGEGGHGVEGGDGGYGVKGGDGVKGGYGGYGARGVREGDGGYGV	390	
Qy	313	-----	312	
Db	391	KEGLREGYGVKEGVGEGDGANAYCARVPRPHRDETTPDAYGAKSGADAYGAKAAPRH	450	
Qy	313	-----	315	
Db	451	RDETSPAYGAKMPRPHRDEASPDTYGAKMPRPHRDETSPDAYGAKMPRPHRAGV	510	
Qy	316	QILYGVNKDEGTWFLVYGAQFSGKDNNSIITRKSFEQGLKIFPGVSBFGKESILFHVTD	375	

Db 511 EVLLGAVRVEGSLFYVGPFGKDNESLSREBFLGGVRMGVQATELAAEAVVLHYTD 570
Qy 376 WVDORPENYREALGDVVDNFNFCPALEFTKKFSEWGNNAFFYFHEHRSSKLLPWPWMG 435
Db 571 WLDADNPVKNREALDDIYGDHNVVCPLMAFQAQRWAGKGVYAYLFDHRSSTLLWPWMG 630
Qy 436 VMHGIEIEFVGLPLERDDNTYTKAEIILSRISIVKRWANFAYGNPNETQNNSTSWPVFKS 495
Db 631 VPHGIEIEFVGLPLERDDNTYTKAEIILSRISIVKRWANFAYGNPNETQNNSTSWPVFKS 689
Qy 496 TEQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAEWENKAGFHRWNNYMM 555
Db 690 SGQRYAHLNARPLSVGHGLRTQICAFWTRFLPKLINATGPPDAERWLEFHRWSSYMG 749
Qy 556 DWKQFNDYTSKKSVCVL 574
Db 750 RWRTOQFEHY-SRQOPCATL 767

RESULT 12
A54413
acetylcholinesterase (EC 3.1.1.7) A precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A54413; T29824
J;Arpagaus, M.; Fedon, Y.; Cousin, X.; Chatonnet, A.; BERGE, J.B.; Fournier, D.; Toutant
R.; Biol. Chem. 269, 9957-9965, 1994
A;Title: cDNA sequence, gene structure, and in vitro expression of ace-1, the gene encoding
A;Reference number: A54413; MUID:94193691; PMID:8144590
A;Accession: A54413
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P38433; GB:X75331; NID:g475060; PIDN:CAA53080.1; PID:g671831
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R;Wu, X.; Le, T.T.
A;Description: The sequence of C. elegans cosmid W09B12.
A;Reference number: Z20693
A;Accession: T29824
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-620 <WUX>
A;Cross-references: EMBL:U58731; PIDN:AAB00593.1; GSPDB:GN00028
A;Experimental source: strain Bristol N2; clone W09B12
C;Genetics:
A;Gene: CESP:ace-1
A;Map position: X
A;Intons: 13/3; 59/2; 154/2; 236/3; 296/2; 454/2; 509/2; 573/1; 606/2
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
F;45-567/Domain: cholinesterase homology <CHE>

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Qy 78 GSEMNPNNTLSEDCLYLNWIPA---PKPKNATVLIWIYGGFGTGTSSLHVYDGKFLA 134
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Qy 195 FGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWATVSLYEARNRTNLAKLTGCS- 253
Db 213 FGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWATVSLYEARNRTNLAKLTGCS- 272
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Db 330 QGNFKTKTQLLAGSNRDESIYFLTYQLPDIFFVAD-FFTKTDFFIKDRQLWKIGVKDILLPRQ 388
Qy 369 IL-----FHYTDWVD-DQSPENYREALGDVVDNFNFCPALEFTKKFSEWGNNAFF 418
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acetylcholinesterase (EC 3.1.1.7) precursor - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66236
R;Anthony, N.; Rocheleau, T.; Mocelin, G.; Lee, H.J.; french-Constant, R.
FEBS Lett. 368, 461-465, 1995
A;Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene f
A;Reference number: S66236; MUID:95361924; PMID:7635199
A;Accession: S66236
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-637 <ANT>
A;Cross-references: UNIPROT:Q9TX11
C;Superfamily: cholinesterase; cholinesterase homology
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F;29-637/Product: acetylcholinesterase #status predicted <MAT>
F;57-594/Domain: cholinesterase homology <CHE>

Query Match 34.4%; Score 1070.5; DB 2; Length 637;
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Qy 62 ANSCCNIDQSFGEHSEMNPNNTLSEDCLYLNWIPA----- 101
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Qy 154 LALP---GNPEAPGNMGLFDQOLALQWQKNIAAFGNPKSVTLFGESAGAASVSLHLLS 210
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Qy 211 PGSHSLFTRAILQSGSFNAPWATVSLYEARNRTNLAKLTGCS-----RENETEIKLRN 266
Db 271 PVTRGLSRRGILQSGTLNAPWHSMAEKALSAEALIDDCNCNVTLLKDNPNYVMNCWRN 330
Qy 267 KDPQOELLNEAFVVPYGTPLSVNFGPTVDGDFLTMDPDIILELQFKKTKTQIILVGNVKDEG 326
Db 331 VDARTISVQO--WNSYSGILGFPSPAPTIDGVFMFTADPMTMLREANLEGVLEILVGSNRDEG 388

